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M protein - protein search, using sw model

run on: March 19, 2004, 11:20:21 ; Search time 17.0916 Seconds
(without alignments)
785.341 Million cell updates/sec

title: US-09-989-903-2
effect score: 1350
sequence: 1 KPDMESEMDPQLQERYD.....KPRKVNPEVQSLRKXLYLQ 260

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 389414 seqs, 51625971 residues

total number of hits satisfying chosen parameters: 389414

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB pep.*
3: /cgn2_6/ptodata/2/iaa/5A COMB pep.*
4: /cgn2_6/ptodata/2/iaa/6A COMB pep.*
5: /cgn2_6/ptodata/2/iaa/6B COMB pep.*
6: /cgn2_6/ptodata/2/iaa/6C COMB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	260	4	US-09-187-789-2
2	1350	100.0	260	4	US-09-139-600-2
3	934.5	69.2	242	4	US-09-187-789-5
4	804.5	59.6	214	4	US-09-187-789-9
5	692.5	51.3	230	4	US-09-187-789-7
6	384	28.4	74	4	US-09-187-789-63
7	384	28.4	74	4	US-09-139-600-58
8	299	22.1	56	4	US-09-187-789-64
9	299	22.1	56	4	US-09-139-600-59
10	280	20.7	53	4	US-09-187-789-65
11	280	20.7	53	4	US-09-139-600-60
12	275.5	20.4	435	5	PCT-US94-07127A-4
13	274.5	20.3	421	4	US-08-983-502-10
14	274.5	20.3	421	5	US-09-516-747-10
15	274.5	20.3	421	5	PCT-US96-10521-10
16	274.5	20.3	435	3	US-08-258-287B-53
17	274.5	20.3	435	3	US-08-368-704C-51
18	274.5	20.3	435	4	US-09-561-756-9
19	274.5	20.3	435	4	US-09-237-721-9
20	274.5	20.3	435	4	US-08-816-075-2
21	274.5	20.3	435	4	US-08-724-378D-9
22	274.5	20.3	435	4	US-09-954-697-9
23	274.5	20.3	441	3	US-08-258-287B-44
24	274.5	20.3	441	3	US-08-368-704C-43
25	274	20.3	277	2	US-08-890-542A-2
26	274	20.3	277	3	US-08-591-605-2
27	274	20.3	277	3	US-08-964-308-6

Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 30, Appli
Sequence 5, Appli
Sequence 30, Appli
Sequence 12, Appli
Sequence 30, Appli
Sequence 11, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-09-187-789-2

; Sequence 2, Application US/09187789

; Patent No. 6340740

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: CASPAGE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING

; FILE REFERENCE: 480140.434C1

; CURRENT APPLICATION NUMBER: US/09/187,789

; CURRENT FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 2

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Mus musculus

; ORGANISM: Mus musculus

; ORGANISM: Mus musculus

; ORGANISM: Mus musculus

; ORGANISM: Mus musculus

; ORGANISM: Mus musculus

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; ORGANISM: Mus musculus

APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
S-09-139-600-2

Query Match 100.0%; Score 1350; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 9.6e-135; Indels 0; Gaps 0;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 KPMSEMSDQPLQERYDMSGARLALTLCTVKAREGSEVDMALERNFRLKFESTMK 60
b 1 KPMSEMSDQPLQERYDMSGARLALTLCTVKAREGSEVDMALERNFRLKFESTMK 60
Y 61 RDPTAQFLELDEFOOTIDNNEEPVSCAFVLMAGHEGLKGEDEKXVLEDLFEVLN 120
b 61 RDPTAQFLELDEFOOTIDNNEEPVSCAFVLMAGHEGLKGEDEKXVLEDLFEVLN 120
Y 121 NKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDEVAVLKNPQSIPT 180
b 121 NKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDEVAVLKNPQSIPT 180
Y 181 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTDVFIHKKSILELTEITRLMANTVWQEG 240
b 181 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTDVFIHKKSILELTEITRLMANTVWQEG 240
Y 241 KPRKVNPEVQSTLRKLYLQ 260
b 241 KPRKVNPEVQSTLRKLYLQ 260

RESULT 3
S-09-187-789-5
Sequence 5, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
S-09-187-789-5

Query Match 69.2%; Score 934.5; DB 4; Length 242;
Best Local Similarity 70.9%; Pred. No. 8.7e-91; Indels 13; Gaps 2;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

Y 8 MSDPQLOERYDMSGARLALTLCTVKAREGSEVDMALERNFRLKFESTMKRDPTAQ 67
b 1 MNPRLSEEEKYDMSGARLALTLCTVKAREGSEVDMALERNFRLKFESTMKRDPTAQ 60
Y 68 FLEELDEFOOTIDNNEEPVSCAFVLMAGHEGLKGEDEKXVLEDLFEVLNNKNCAL 127
b 61 FQEELEKFOQALDSREDPVSCAFVLMAGHEGLKGEDEKXVLEDLFEVLNNKNCAL 120
Y 128 RGPVKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDEVAVLKNPQSIPTYTDLHI 186

APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 230

Db 121 RAKPKVYIIQACRGEHRDPG-----ETVGGDEIVVMVKDSPTIPTYTDALHV 168
QY 187 YSTVEGYLSYRDEKSGSFIQTLTDVFIHKKSILELTEITRLMANTVWQEGKPKVN 246
Db 169 YSTVEGYIAYRHDQKSGCFIQTLDVDFVTKRKHILELLTEVTRMAEALVQEGKARKTN 228
QY 247 PEVQSTLRKLYLQ 260
Db 229 PEIQSTLRKRLYLQ 242

RESULT 4
US-09-187-789-9
Sequence 9, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-9

Query Match 59.6%; Score 804.5; DB 4; Length 214;
Best Local Similarity 63.0%; Pred. No. 4.2e-77; Indels 41; Gaps 3;
Matches 160; Conservative 27; Mismatches 26; Indels 41; Gaps 3;

QY 8 MSDPQLOERYDMSGARLALTLCTVKAREGSEVDMALERNFRLKFESTMKRDPTAQ 67
Db 1 MNPRLSEEEKYDMSGARLALTLCTVKAREGSE-----ETVGGDEIVVMVKDSPTIPTYTDALHV 140
QY 68 FLEELDEFOOTIDNNEEPVSCAFVLMAGHEGLKGEDEKXVLEDLFEVLNNKNCAL 127
Db 35 --ELEEKFOQALDSREDPVSCAFVLMAGHEGLKGEDEKXVLEDLFEVLNNKNCAL 92
QY 128 RGPVKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDEVAVLKNPQSIPTYTDLHI 186
Db 93 RAKPKVYIIQACRGEHRDPG-----ETVGGDEIVVMVKDSPTIPTYTDALHV 140
QY 187 YSTVEGYLSYRDEKSGSFIQTLTDVFIHKKSILELTEITRLMANTVWQEGKPKVN 246
Db 141 YSTVEGYIAYRHDQKSGCFIQTLDVDFVTKRKHILELLTEVTRMAEALVQEGKARKTN 200
QY 247 PEVQSTLRKLYLQ 260
Db 201 PEIQSTLRKRLYLQ 214

RESULT 5
US-09-187-789-7
Sequence 7, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 230

```
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-7

Query Match      51.3%; Score 692.5; DB 4; Length 230;
Best Local Similarity 72.0%; Pred. No. 3.4e-65;
Matches 134; Conservative 22; Mismatches 17; Indels 13; Gaps 2;

QY 8 MSDPQLOEYRDMGASLALTLCTVKAREGSEVDMALERMPYLFKFESTMKRDPTAQ 67
DB 1 MENPSLEEKYDMGASLALTLCTVKAREGSEEDLDALEHMFQLFESTMKRDPTAQ 60
QY 68 FLEELDEFQQTIDNWEFVSCAFVVLMAHGSEGLLKGDEKMWLEDLFEVLNNKCKAL 127
DB 61 FQEELEKFAIDSRDFVSCAFVVLMAHGREGPLKGEDGEMVLENLFEALNNKNCQAL 120
QY 128 RQPKVYIIQACRGHRDPGSELGRNVEELGGDEBELGGDE-VAVLKNPQSIPTTDLHI 186
DB 121 RAKPKVYIIQACRGHRDPG-----ETVGGDEIVMWIKDSPQTIPTTDLHV 168
QY 187 YSTVEG 192
DB 169 YSTVEG 174

RESULT 6
US-09-187-789-63
; Sequence 63, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 63
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-63

Query Match      28.4%; Score 384; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.9e-33;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AREGSEVDMALERMPYLFKFESTMKRDPTAQOQFLEELDEFQQTIDNWEFVSCAFVVL 94
DB 1 AREGSEVDMALERMPYLFKFESTMKRDPTAQOQFLEELDEFQQTIDNWEFVSCAFVVL 60
QY 95 AHGEGLLKGEDEK 108
DB 61 AHGEGLLKGEDEK 74

RESULT 7
US-09-139-600-58
; Sequence 58, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-58

Query Match      22.1%; Score 299; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MYRLEDLFEVLNNKCKALRGKPKVYIIQACRGHRDPGSELGRNVEELGGDEELGG 164
DB 1 MYRLEDLFEVLNNKCKALRGKPKVYIIQACRGHRDPGSELGRNVEELGGDEELGG 56

RESULT 9
US-09-139-600-59
; Sequence 59, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-59

Query Match      22.1%; Score 299; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MYRLEDLFEVLNNKCKALRGKPKVYIIQACRGHRDPGSELGRNVEELGGDEELGG 164
DB 1 MYRLEDLFEVLNNKCKALRGKPKVYIIQACRGHRDPGSELGRNVEELGGDEELGG 56
```

db 1 MVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPGEELRGNEELGDEELGG 56

RESULT 10

JS-09-187-789-65
Sequence 65, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 65
LENGTH: 53
TYPE: PRT
ORGANISM: Mus musculus
JS-09-187-789-65

Query Match 20.7%; Score 280; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e-22;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 165 DEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIHKK 217
|||||
db 1 DEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIHKK 53

RESULT 11

JS-09-139-600-60
Sequence 60, Application US/09139600
Patent No. 6432628
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHOD OF USE
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 53
TYPE: PRT
ORGANISM: Mus musculus
JS-09-139-600-60

Query Match 20.7%; Score 280; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e-22;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 165 DEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIHKK 217
|||||
b 1 DEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIHKK 53

RESULT 12

CT-US94-07127A-4
Sequence 4, Application PC/TUS9407127A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Interleukin-1 Converting Enzyme Like Apoptosis Protease-1, an
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND

STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07127A
FILING DATE: submitted herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR 2
MOLECULE TYPE: PROTEIN
PCT-US94-07127A-4

Query Match 20.4%; Score 275.5; DB 5; Length 435;
Best Local Similarity 29.6%; Pred. No. 1.3e-20;
Matches 68; Conservative 53; Mismatches 100; Indels 9; Gaps 4;

Qy 36 REGSEVDMEALERMFYLLKFESTMKRDTAQOFLFELDFEQTTIDNNEEPYSCAFVILMA 95
Db 202 RSGGDVDSHTLVTLFKLLGYDVHVLCDQTAGEKELQNFAQ-LPAHRVTDS-IVALLS 259
Qy 96 HGEGLLKGEDEKMWRLDELFEVLANNKCKALRGKPKVYIIQACRGEHRDPGEELRGNEE 155
Db 260 HGVEGAIYGVGKLIQLQEVFOLFDFNANCPSLQNKPKMFFQACRGEHDTDRGVQDQGN 319
Qy 156 LGGDEBELGGDEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRHDKEKSGFGTQLTLDVFIH 215
Db 320 HAGSPCEESDAGKELPKMRDLPTRSDMICGYACLGTAAMNTRGSGWYIEALAQVF-S 378
Qy 216 KXGSILELTEEITRLMANTVYMQEKKPR-----KVNPEVQSTLRKKLYL 259
Db 379 ERGCDMHVADMLVKVNALIKOREGVAPGTGFHRCCKEMSEYCGSTLCRHYL 428

RESULT 13

US-08-983-502-10
Sequence 10, Application US/08983502
Patent No. 6399327
GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yuri V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-502-10

Query Match 20.3%; Score 274.5; DB 4; Length 421;
Best Local Similarity 29.7%; Pred. No. 1.6e-20;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;
QY 36 REGSEVDMERALERMFRLKPFSTMKRDPTAQOFLBELDEFQQTIDNWEPEVSCAFVVLMA 95
Db 188 RSGGDVHSTLTFLKLGVDVHVLCDTAQEMQEKLNFAQ-LPAHRVTDSC-IVALLS 245
QY 96 HGEGLLKGEDEKMWRLDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGSELRGNEE 155
Db 246 HGVEGAIYGVGDKLLQLOEVFQFNANCPSLQNKPKMFFIQAQCRGDETDGRGVDDQDGN 305
QY 156 LGGDEELGDEVAVLKNNPQSIPTVTDTHIYSTVEGVLVSRHDEKSGFTQTLTDVFIH 215
Db 306 HAGSPCEESDAGKELPKMRFLPFRSDMICGYACLKGTAAAMNTKSGSWYIEALAQVFE 365
QY 216 KGGS--ILELTEITRLMANTVMOEGKP---RKNVPEVQSTLRKLYL 259
Db 366 RACDMEHADMVKNVALIKDRGYAPGTEFFHRCKEMSEYCSYTLCHRLYL 414

RESULT 14
US-09-516-747-10
Sequence 10, Application US/09516747
Patent No. 6586571
GENERAL INFORMATION:
APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya M. GONCHAROV
Yury V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,747
FILING DATE: 01-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/983,502
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-516-747-10

Query Match 20.3%; Score 274.5; DB 4; Length 421;
Best Local Similarity 29.7%; Pred. No. 1.6e-20;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;
QY 36 REGSEVDMERALERMFRLKPFSTMKRDPTAQOFLBELDEFQQTIDNWEPEVSCAFVVLMA 95
Db 188 RSGGDVHSTLTFLKLGVDVHVLCDTAQEMQEKLNFAQ-LPAHRVTDSC-IVALLS 245
QY 96 HGEGLLKGEDEKMWRLDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGSELRGNEE 155
Db 246 HGVEGAIYGVGDKLLQLOEVFQFNANCPSLQNKPKMFFIQAQCRGDETDGRGVDDQDGN 305
QY 156 LGGDEELGDEVAVLKNNPQSIPTVTDTHIYSTVEGVLVSRHDEKSGFTQTLTDVFIH 215
Db 306 HAGSPCEESDAGKELPKMRFLPFRSDMICGYACLKGTAAAMNTKSGSWYIEALAQVFE 365
QY 216 KGGS--ILELTEITRLMANTVMOEGKP---RKNVPEVQSTLRKLYL 259
Db 366 RACDMEHADMVKNVALIKDRGYAPGTEFFHRCKEMSEYCSYTLCHRLYL 414

RESULT 15
PCT-US96-10521-10
Sequence 10, Application PC/TUS9610521
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34

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/ NUMBER OF SEQUENCES: 34
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/10521
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 114,615
/ FILING DATE: 16-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 114,986
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 115,319
/ FILING DATE: 14-SEP-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 116,588
/ FILING DATE: 27-DEC-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IL 117,932
/ FILING DATE: 16-APR-1996
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 421 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ CT-US96-10521-10

Query Match      20.3%; Score 274.5; DB 5; Length 421;
Best Local Similarity 29.7%; Pred. No. 1.6e-20;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;

2Y 36 REGSEVDMEALERMFYLFKESTWKRDPDTAQQLLELDSEFQQTIDNWEEFVSCAFVILMA 95
Db 188 RSGGDVDHSTLVTLFVLKLGIDVHVLCDTAQEMQEKLNPAQ-LPAHRVTDSQ-IVALLS 245
2Y 96 HGEGLLKGEDEKMRLEDLFVLNNKNKALRGKPKYIIQACRGEHRDPGEELRGNEE 155
Db 246 HGEVGIYGVGKLLQLEVFQLFQFNANCPSLQNKPKMFFIQACRGDETDGRGVDDQDGKN 305
2Y 156 LGDBEELGDEVAVLKNNPQSIPTTYTDLHIYSTVEGYLSYRDEKSGSFIQTITDVFH 215
Db 306 HAGSPGCEESDAGKEKLPKMRPLPTRSDMICGYACLGTAAMRNTRKGSWYIEALAQVFSE 365
2Y 216 KKGS--ILELTEEITRLMANTENVQEGKP---RKVNPEVQSTLRKKLYL 259
Db 366 RACDMHVADMLVKVNALIKDREGVAPGTETHRCKEMSEYCVSTLCRHLYL 414
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Search completed: March 19, 2004, 11:25:36
Job time : 18.0916 secs

GenCore version 5.1.6
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* protein - protein search, using sw model

on on: March 19, 2004, 11:17:55 ; Search time 37.2908 seconds

(without alignments)
2199.863 Million cell updates/sec

itle: US-09-989-903-2

effect score: 1350

sequence: 1 KPDMESEMSDPLQEEYD.....XPRKVNPEVQTLRKKLYLQ 260

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

earched: 1017041 seqs, 315518202 residues

otal number of hits satisfying chosen parameters: 1017041

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	235.5	21.9	423	Q91B67	Q91B67 xenopus lae
2	279.5	20.7	452	Q8C9H7	Q8C9H7 mus musculus
3	278	20.6	318	Q91B65	Q91B65 xenopus lae
4	278	20.6	403	Q90WU0	Q90WU0 gallus gall
5	277	20.5	277	Q8MJU1	Q8MJU1 felis silve
6	276.5	20.5	452	Q8K241	Q8K241 mus musculus
7	276	20.4	313	Q8CHV5	Q8CHV5 mus musculus
8	274.5	20.3	435	Q9BUP7	Q9BUP7 homo sapien
9	274.5	20.3	452	Q55194	Q55194 rattus norv
10	273	20.2	277	Q95ND5	Q95ND5 sus scrofa
11	270.5	20.0	277	Q8MKI5	Q8MKI5 canis faml
12	266	19.7	277	Q8MJC3	Q8MJC3 oryctolagus
13	266	19.7	282	Q98UI8	Q98UI8 brachydanio
14	266	19.7	454	Q9R0T0	Q9R0T0 mus musculus
15	264.5	19.6	303	Q88550	Q88550 rattus norv
16	263	19.5	453	Q8C3Q0	Q8C3Q0 mus musculus

17	263	19.5	454	11	Q8C3Q9	Q8C3Q9 mus musculus
18	261.5	19.4	316	5	Q817B0	Q817B0 geodia cydo
19	261.5	19.4	426	5	Q816Y2	Q816Y2 geodia cydo
20	255	18.9	454	11	Q90HK1	Q90HK1 rattus norv
21	254	18.8	399	13	Q91B63	Q91B63 xenopus lae
22	253	18.7	280	13	Q8JIS9	Q8JIS9 oryzias lat
23	253	18.7	283	13	Q93417	Q93417 gallus gall
24	253	18.7	289	5	Q86PU0	Q86PU0 anopheles s
25	252	18.7	302	13	Q918S9	Q918S9 oncorhynch
26	250	18.5	280	13	Q8JCM9	Q8JCM9 fugu rubrip
27	250	18.5	290	13	Q8JIS8	Q8JIS8 oryzias lat
28	249	18.4	280	13	Q8UG42	Q8J942 fugu rubrip
29	246	18.2	182	6	O7623	O7623 ovis aries
30	245.5	18.2	476	13	Q918J3	Q918J3 brachydanio
31	241.5	17.9	328	5	Q81TP3	Q81TP3 branchiosto
32	241	17.9	304	13	Q93415	Q93415 gallus gall
33	241	17.9	482	11	Q9JHX4	Q9JHX4 rattus norv
34	240.5	17.8	520	13	Q91B62	Q91B62 xenopus lae
35	238	17.6	417	5	Q91IU6	Q91IU6 pristionchu
36	237	17.6	276	11	Q9D089	Q9D089 mus musculu
37	236.5	17.5	293	5	Q819V7	Q819V7 bombyx mori
38	236	17.5	189	11	Q8BNT4	Q8BNT4 mus musculu
39	234.5	17.4	482	13	Q90WU1	Q90WU1 gallus gall
40	234	17.3	276	11	Q9M47	Q9M47 mus musculu
41	233.5	17.3	277	11	Q35397	Q35397 rattus norv
42	232	17.2	383	13	Q919L7	Q919L7 brachydanio
43	232	17.2	415	13	Q801M6	Q801M6 xenopus lae
44	229	17.2	419	13	Q7ZXD2	Q7ZXD2 xenopus lae
45	229	17.0	283	13	O42284	O42284 gallus gall

ALIGNMENTS

RESULT 1

Q91B67	PRELIMINARY;	PRT;	423 AA.
ID	Q91B67		
AC	Q91B67		
DT	01-OCT-2000 (TRENBLrel. 15, Created)		
DT	01-OCT-2000 (TRENBLrel. 15, Last sequence update)		
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)		
DE	Caspase-2.		
GN	XCASPAGE-2.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=20209426; PubMed=10744739;		
RX	Nakajima K., Takahashi A., Yaoita Y.;		
RA	"Structure, expression and function of the Xenopus laevis caspase		
RT	family.";		
RL	J. Biol. Chem. 275:10484-10491(2000).		
DR	EMBL; AB038168; BAA94746.1;		
DR	HSSP; P29466; LICE.		
DR	MEROPS; C14.006; -.		
DR	GO; GO:0005622; C:intracellular; IEA.		
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.		
DR	GO; GO:0030693; F:caspase activity; IEA.		
DR	GO; GO:0006915; P:apoptosis; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR001315; CARD.		
DR	InterPro; IPR002138; ICE_p10.		
DR	InterPro; IPR001309; ICE_p20.		
DR	InterPro; IPR002398; Peptidase_C14.		
DR	Fam; PF00656; Peptidase_C14; 1.		
DR	PRINTS; PR00376; ILIHCENZYME.		
DR	SMART; SM00114; CARD; 1.		
DR	SMART; SM00115; CASC; 1.		
DR	PROSITE; PS50209; CARD; 1.		

R PROSITE; PS01122; CASPASE_CYS; 1.
 R PROSITE; PS01121; CASPASE_HIS; 1.
 R PROSITE; PS0207; CASPASE_P10; 1.
 R PROSITE; PS0208; CASPASE_P20; 1.
 Q SEQUENCE 423 AA; 47123 MW; E31EB1FD133F01FD CRC64;
 Query Match 21.9%; Score 295.5; DB 13; Length 423;
 Best Local Similarity 27.0%; Pred. No. 4.5e-17;
 Matches 84; Conservative 58; Mismatches 104; Indels 65; Gaps 10;
 Y 2 PMSEMSDP-----QPLQERYDMSCARLALTLIC-----VTKARE----- 37
 b 114 PQESTLSRPGRCQCREYRESIDGPGVTVQLCSNFVTHCOAYKMSHSCPRGRALL 173
 Y 38 -----GSEVDMEALERNFRYLKPESTMKRDPDTAQOFLBELDEFOOTIDNWEVPVSCAFVLA 95
 b 174 ISNVKFPDPDLYRCGGEVDLASLEKLFSSLGVCVDRCNLAQSMNSQLGAFSAL----- 229
 Y 83 BEPVSCAF-----VVMARHGEGLIKGDEKMWRLDLFEVLNNKNCALRGKPKVYIIQA 138
 b 230 --PVHSALDSCVALLSHGLDGVYTGDKLVQLQEVFTALDNHCPQLONKPKFFIOA 287
 Y 139 CRGEHRDGEELRGNELGG-----DEELGGDEVALKNNPQSIPTVTTTLHIYSTVEGY 193
 b 288 CRGETDRGVORDRGEGSQSPGCEQSDAGREDIKV-----RLPTQSDMICAYACLKGT 341
 Y 194 LSYRDEKSGSFIQTLTDVFI-HKKGK--ILELTEEITRLMANTENVQEGKP---RKVNPE 248
 b 342 VSLRNTKGSWFQDLYSVFSQHSKDTHVADMLVKVNALIKEREHGFOTEFHRCCKENSE 401
 Y 249 VQSTLRKKLYL 259
 b 402 YCSTLCRLDLYL 412

RESULT 2
 Q8C9H7 PRELIMINARY; PRT; 452 AA.
 D Q8C9H7
 C Q8C9H7
 Y 01-MAR-2003 (TRENBLrel. 23, Created)
 Y 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 Y 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Caspase 2.
 IN CASP2.
 XS Mus musculus (Mouse).
 XC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 XC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 XX NCBI_TaxID=10090;
 YN [1]
 YN SEQUENCE FROM N.A.
 YN STRAIN=C57BL/6J; TISSUE=Thymus;
 YN MEDLINE=22354683; PubMed=12466851;
 YN The FANTOM Consortium,
 YN the RIKEN Genome Exploration Research Group Phase I & II Team;
 YN "Analysis of the mouse transcriptome based on functional annotation of
 YN 60,770 full-length cDNAs";
 YN Nature 420:563-573(2002).
 YN EMBL; AK042072; BAC31153.1; -.
 YN MGD; MGI:97295; Casp2.
 YN GO; GO:0005622; C:intracellular; IEA.
 YN GO; GO:0016329; F:apoptosis regulator activity; IEA.
 YN GO; GO:0030593; F:caspase activity; IEA.
 YN GO; GO:0006915; P:apoptosis; IEA.
 YN GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 YN InterPro; IPR001315; CARD.
 YN InterPro; IPR002138; ICE_P10.
 YN InterPro; IPR001309; ICE_P20.
 YN InterPro; IPR002398; Peptidase_C14.
 YN Pfam; PF00619; CARD; 1.
 YN PRINTS; PR00376; ILIBENZYM.
 YN SMART; SM00114; CARD; 1.
 YN SMART; SM00115; CASC; 1.

DR PROSITE; PS0209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS0208; CASPASE_P20; 1.
 SQ SEQUENCE 452 AA; 50889 MW; C3715908508619CA CRC64;
 Query Match 20.7%; Score 279.5; DB 11; Length 452;
 Best Local Similarity 31.0%; Pred. No. 1.2e-15;
 Matches 72; Conservative 52; Mismatches 95; Indels 13; Gaps 6;
 QY 36 RGSSEVDMEALERNFRYLKPESTMKRDPDTAQOFLBELDEFOOTIDNWEVPVSCAFVLA 95
 Db 219 RSGVDVHTLVTLLRGVNVHVLHDTAQEQEKLQNPQA--LPAHRVTDSCV-VALLS 276
 QY 96 HGEELGLKGEDEKMWRLDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPG---BELRG 152
 Db 277 HGVGGIGVGDGKLLQEQEVRFLFDNANCPSLQNKPKMFFIACRGEHDTDRGVDDQDGN 336
 QY 153 NEELGGDEELGGDEVALKNNPQSIPTVTTTLHIYSTVEGYLSYRDEKSGSFIQTLTDV 212
 Db 337 HQSPGCEESDAGKEELMK---MLPTQSDMICAYACLKGNAMRNTRKGSWYIEALTQV 393
 QY 213 FHKKGK--ILELTEEITRLMANTENVQEGKP---RKVNPEVQSTLRKKLYL 259
 Db 394 FSEACDMFVADMLVKVNALIKEREHGFOTEFHRCCKENSEYCSLCCQLLYL 445
 RESULT 3
 Q9IB65 PRELIMINARY; PRT; 318 AA.
 AC Q9IB65
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Caspase-7.
 GN XCASPASE-7.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 CX NCBI_TaxID=8355;
 RN [1]
 RN SEQUENCE FROM N.A.
 RL MEDLINE=20209426; PubMed=10744739;
 RX Nakajima K., Takahashi A., Yacita Y.;
 RT "Structure, expression and function of the Xenopus laevis caspase
 RT family";
 RL J. Biol. Chem. 275:10484-10491(2000).
 DR EMBL; AB038170; BAA94748.1; -.
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.004; -.
 DR GO; GO:0030593; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00656; Peptidase_C14.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS0208; CASPASE_P20; 1.
 SQ SEQUENCE 318 AA; 35937 MW; 6EBC6684AF68A128 CRC64;
 Query Match 20.6%; Score 278; DB 13; Length 318;
 Best Local Similarity 32.9%; Pred. No. 9.9e-16;
 Matches 77; Conservative 39; Mismatches 96; Indels 22; Gaps 7;
 QY 35 AREGSEVDMEALERNFRYLKPESTMKRDPDTAQOFLBELDEFOOTIDNWEVPVSCAFV 93
 Db 97 ARNGTDDIDARELLRCFKGLGFDVNVNNKSC---EEMENLRTVAQQDHKDSACFACIF 152

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14 94 MAMGEGLKGEDEKVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGSELGN 153
15 153 LSHGEGLIYGTGAM-PIKVLITLPRGDCNCRSLVCKPKLFIQACRGEHFDG----- 205
16 154 EEGLGDEELGGDEVAVLKNPQSIPTVDTLHYSYVEGYSYRDEKSGHFIQTLTVF 213
17 206 --LEADSGSVNDSLETDPANRHKIPVEADFLYASTVPGYVWRNPGMGSNFVQALCSV- 262
18 214 IHKKGSIETEETTR---LMANTEVMOEGKP---RKVNPEVOSTLRKKLYLQ 260
19 263 LNEYKKEVNLQILTRVNLVATQFESYSDDPQFSKKKQIPCVWSMLTKELYFK 316
20
21 RESULT 4
22 ID Q90WU0 PRELIMINARY; PRT; 403 AA.
23 AC Q90WU0;
24 DT 01-DEC-2001 (TREMELrel. 19, Created)
25 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
26 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
27 DE Caspase 9 (Fragment)
28 OS Gallus gallus (Chicken)
29 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
30 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
31 OC Gallus.
32 NCBI_TaxID=9031;
33 RN [1]
34 RP SEQUENCE FROM N.A.
35 RA Bampton J., Bridgham J., Johnson A.L.;
36 RT "Caspase-8 and -9 expression in the hen ovary.";
37 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
38 EMBL; AY057940; AAL23701.1;
39 DR GO; GO:0005622; C:intracellular; IEA.
40 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
41 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
42 DR GO; GO:0005488; F:binding; IEA.
43 DR GO; GO:0030693; F:caspase activity; IEA.
44 DR GO; GO:0006915; F:apoptosis; IEA.
45 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
46 DR GO; GO:0006810; P:transport; IEA.
47 DR InterPro; IPR001315; CARD.
48 DR InterPro; IPR002138; ICE_p10.
49 DR InterPro; IPR001309; ICE_p20.
50 DR InterPro; IPR001993; Mitoch carrier.
51 DR InterPro; IPR002398; Peptidase_C14.
52 DR Pfam; PF00619; CARD; 1.
53 DR Pfam; PF00656; Peptidase_C14; 1.
54 DR PRINTS; PR00376; ILIBCNZYME.
55 DR SMART; SM00115; CASC; 1.
56 DR PROSITE; PS01122; CASPASE_CYS; 1.
57 DR PROSITE; PS01121; CASPASE_HIS; 1.
58 DR PROSITE; PS02027; CASPASE_P10; 1.
59 DR PROSITE; PS02028; CASPASE_P20; 1.
60 DR PROSITE; PS00215; MITOCH_CARRIER; 1.
61 FT NON_TER
62 SQ SEQUENCE 403 AA; 44913 MW; 0F1E40C3E6594FC4 CRC64;
63
64 Query Match 20.6%; Score 278; DB 13; Length 403;
65 Best Local Similarity 28.2%; Pred. No. 1.4e-15;
66 Matches 87; Conservative 44; Mismatches 106; Indels 72; Gaps 9;
67
68 QY 1 KPDMSEMSDPPQLEERYDMSGARLALTLCV-----TYAREGSE 40
69 DB 112 QPESERFRMPAPAGSVAQSDKSRPTDWCSTCEQTPCGHCLFNVSFSDLSSTRAGSD 171
70
71 QY 41 VQMEALERFRYLKFKSTWKDPDQAQFLELDEFQOTIDNWEPPVSCAFVLMHAGEE- 99
72 DB 172 IDCEKLEKFRSLCFHVTLRMLKQEDVLRKLAR-LDH--SALDCCLVILSHGCGT 228
73
74 QY 100 -----GLKGEDEKVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGSEL--- 150
75 DB 229 SHIQPPGGYGTGDKTIPIERIVNFGSQPSLRGKPKLFFIQACGGEQKDGQFEVDCE 288
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151 151 -----RGNEELGGDEELGGDEVAVLKNPQSIPTVDTLHYSY 189
152 DB 289 SPQDETCRRSIESDAIPFOAPSGNE---DEP---DAVA-----SLTPGDILVSYST 334
153 QY 190 VEGYLSYRDEKSGHFIQTLTVFTHKKGSIETEETRLMANTEVMOEGKPKVKNPEV 249
154 DB 335 PFGVSVWRDKVSGSVETLDSVLEHYARS-----EDLTKLRLVSDIVSSGKRYKQIPGC 390
155 QY 250 QSTRKKLY 258
156 DB 391 FNFELRKKIF 399
157
158 RESULT 5
159 ID Q8MJU1 PRELIMINARY; PRT; 277 AA.
160 AC Q8MJU1;
161 DT 01-OCT-2002 (TREMELrel. 22, Created)
162 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
163 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
164 DE Caspase3.
165 OS Felis silvestris catus (Cat).
166 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
167 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
168 NCBI_TaxID=9685;
169 RN [1]
170 RP SEQUENCE FROM N.A.
171 RA Yamazaki J., Sano J., Kano R., Hasegawa A.;
172 RT "Felis catus mRNA for caspase3, complete cds.";
173 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
174 EMBL; AB090246; BAC10589.1;
175 DR GO; GO:0030693; F:caspase activity; IEA.
176 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
177 DR InterPro; IPR002138; ICE_p10.
178 DR InterPro; IPR001309; ICE_p20.
179 DR InterPro; IPR002398; Peptidase_C14.
180 DR Pfam; PF00656; Peptidase_C14; 1.
181 DR PRINTS; PR00376; ILIBCNZYME.
182 DR SMART; SM00115; CASC; 1.
183 DR PROSITE; PS01122; CASPASE_CYS; 1.
184 DR PROSITE; PS01121; CASPASE_HIS; 1.
185 DR PROSITE; PS02027; CASPASE_P10; 1.
186 DR PROSITE; PS02028; CASPASE_P20; 1.
187 SQ SEQUENCE 277 AA; 31465 MW; 8749679C30AB46F6 CRC64;
188
189 Query Match 20.5%; Score 277; DB 6; Length 277;
190 Best Local Similarity 30.5%; Pred. No. 1e-15;
191 Matches 84; Conservative 40; Mismatches 105; Indels 46; Gaps 9;
192
193 QY 6 SEMSDPPQLEERYDMSGARLALTLCVTK-----ARGSEVDMEALERMFRYLFK 55
194 DB 24 SKMSDSGYMDSYKMDYPMGLCIINNNKNFHESTGMPFSRSGTDYDAANLRETFTNLKY 83
195 QY 56 ESTWKRPDPTAQFLELDEFQOTIDNWEPPVSCAFVLMHAGEEGLKGEDEKVRLEDL 115
196 DB 84 EVRNKNDLREQIVALLDSVSRDEHKKRSFIC---VLSSHGEGLIYGTNGP-VDLKKL 139
197 QY 116 FEVLNNKNCALRGKPKVYIIQACRGEHRDPGSELRGNEELGGDEELGGDEVAVLKNPQ 175
198 DB 140 TGFFRGDYCRSLTGKPKLFIQACRGTELDGCIETDSGTE-----DDIAC-----Q 185
199 QY 176 SIPTVDTLHYSYVEGYSYRDEKSGHFIQTLTVFTHKKGSIETEETRLMA 232
200 DB 186 KIPVEADFLYASTVPGYVWRNPKGSGWFIQSLCMLRLYAHE----LEFMHLIRV-- 239
201 QY 233 NTEVMOEGKP-----RKVNPEVOSTLRKKLY 258
202 DB 240 NRKVATEFESFSLDSAFHGKKQIPCVISMLTKELY 274
203
204 RESULT 6
205 Q8K241
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R GO; GO:0005622; C:intracellular; IEA.
R GO; GO:0016329; F:apoptosis regulator activity; IEA.
R GO; GO:0030693; F:caspase activity; IEA.
R GO; GO:0008233; F:peptidase activity; IEA.
R GO; GO:0006915; P:apoptosis; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR001315; CARD.
R InterPro; IPR002138; ICE_P10.
R InterPro; IPR001309; ICE_P20.
R InterPro; IPR002398; Peptidase_C14.
R Pfam; PF00619; CARD; 1.
R PRINTS; PR00376; IL1BCENZYM.
R SMART; SM00114; CARD; 1.
R SMART; SM00115; CARD; 1.
R PROSITE; PS0209; CARD; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS0207; CASPASE_P10; 1.
R PROSITE; PS0208; CASPASE_P20; 1.
R PROSITE; PS0208; CASPASE_P20; 1.
R PROTEASE.
W Q SEQUENCE 435 AA; 48869 MW; 10CFASALF9369E57 CRC64;

Query Match 20.3%; Score 274.5; DB 4; Length 435;
Best Local Similarity 29.7%; Pred. No. 38-15;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;

Y 36 REGSEVMEALERMFRYLKFESTMKRDPTAQOFLBELDEFOQTIDNWEVPVSCAFVVLMA 95
b 202 RSGGDVHSLVTLFKLLGYDVHVLCDQTAEQMKLQNFQA-LPAHRVTDSC-IVALLS 259
Y 96 HGEGLKGEDEKQVRLDELFEVLNNKNCALRGKPKVYIIQACRGEHRDGESELRGNEE 155
b 260 HGVEGAIYGVGKLLQLOEVLFDNANCPSLQNKPKMFFIQACRGEHTRDGRVQDQDGN 319
Y 156 LGDEELGGDEAVLKNPQSIPTVTDTHLYSTVEGYSYRDEKSGSGFTQTLTDVFIH 215
b 320 HSGPCEESDAKELPKWRLPTSDMTCGACILKGNAMNTRKGSWYIEALAQVFE 379
Y 216 KKGSG--ILELTETRLMANTVMOGKPK---RKVNPEVQSTLRKKLYL 259
b 380 RACDMHVMADMLKVNALIKREGYAPGTFFHRCCKEMSEYCSYCTLCRLHLYL 428

RESULT 9
O55194 PRELIMINARY; PRT; 452 AA.
O55194
Y 01-JUN-1998 (TrEMBLrel. 06, Created)
Y 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
Y 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Y NEDD2/ICH-1.
R Rattus norvegicus (Rat).
X Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
X Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
X NCBI_TaxID=10116;
X [1]
X SEQUENCE FROM N.A.
X MEDLINE=9807427; PubMed=9427555;
X Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.;
X "Cloning and expression of the cDNA encoding rat caspase-2.";
X Gene 202:127-132(1997).
X [2]
X SEQUENCE FROM N.A.
X STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
X Jin K.L., Simon R.P., Graham S.H.;
X Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
X EMBL; U77933; AAB96379.1; --
X EMBL; AF136231; AAD33684.1; --
X PIR; JC6507; JC6507.
X HSSP; P29466; 1ICE.
X GO; GO:0005622; C:intracellular; IEA.
X GO; GO:0016329; F:apoptosis regulator activity; IEA.

DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50728 MW; 03F9D096BB741CE3 CRC64;

Query Match 20.3%; Score 274.5; DB 11; Length 452;
Best Local Similarity 30.6%; Pred. No. 3-2e-15;
Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

QY 36 REGSEVMEALERMFRYLKFESTMKRDPTAQOFLBELDEFOQTIDNWEVPVSCAFVVLMA 95
Db 219 RSGGDVHSLVTLFKLLGYDVHVLCDQTAEQMKLQNFQA-LPAHRVTDSC-IVALLS 276
QY 96 HGEGLKGEDEKQVRLDELFEVLNNKNCALRGKPKVYIIQACRGEHRDGP---EELRG 152
Db 277 HGVEGAIYGVGKLLQLOEVLFDNANCPSLQNKPKMFFIQACRGEHTRDGRVQDQDGN 336
QY 153 NRELGGDEELGGDEAVLKNPQSIPTVTDTHLYSTVEGYSYRDEKSGSGFTQTLTDV 212
Db 337 HSGPCEESDAKELPKWRLPTSDMTCGACILKGNAMNTRKGSWYIEALAQV 393
QY 213 FHKKGS--ILELTETRLMANTVMOGKPK---RKVNPEVQSTLRKKLYL 259
Db 394 FSERACDMHVMADMLKVNALIKREGYAPGTFFHRCCKEMSEYCSYCTLCQQLYL 445

RESULT 10
Q95ND5 PRELIMINARY; PRT; 277 AA.
AC Q95ND5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21334413; PubMed=11440638;
RX Muneta Y., Shimojima Y., Mori Y.;
RA "Porcine caspase-3: cloning and its activity during apoptosis of
RT porcine PK15 cells induced by porcine Fas-ligand.";
RL J. Interferon Cytokine Res. 21:409-415(2001).
DR EMBL; AB029345; BAB55544.1; --
DR MROPS; C14.003; --
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.

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Q SEQUENCE 277 AA; 31379 MW; 616COF56141B012B CRC64;
Query Match 20.2%; Score 273; DB 6; Length 277;
Best Local Similarity 31.8%; Pred. No. 2.2e-15;
Matches 83; Conservative 34; Mismatches 100; Indels 44; Gaps 9;
Y 19 YDMSGARLALTLCVTK-----AREGSEVDMEALRMFRYLKFSTWKRDPDTAQOF 68
b 37 YKDYDPEMGLCIINNNKFNKNTGACRSGTDVDAANLRETFTNLKYEVNRKNDLTR--- 93
Y 69 LEELDFEFOOTIDNWEFVSCAFV-VLMAHGEGLKGEDEKMWLEDFEVLNNKNCKAL 127
b 94 -EILELMSVSKEDHSKRSSFICVLISGEKGKIFGTNGP-VDLKLTSTFRGDCRRL 151
Y 128 RGPKPVYIQAQGEHRDPGEELRGNEELGDEELGDEVAVLKNNPOSIFTYDTLHIY 187
b 152 TGRPKLFIQAQCGTDLDCGIETDSGTE-----DDMAC-----QKIPVEADFLYAY 197
Y 188 STVEGYSYRHDKEGSGFTQTLTDV---FIHKKSILELTTEITELMANTVMQEG--- 240
b 198 STAPGYYSWRNSKDGSWFQSLCAALKQYVHK-----LELMHILTRVNRKVAEFESFSTD 253
Y 241 ---KPRKVNPEVOSTLRKKLY 258
b 254 STHAKQIPICVISMLTKELY 274
D Q8MKI5 PRELIMINARY; PRT; 277 AA.
T 01-OCT-2002 (TREMBlrel. 22, Created)
T 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
T 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
S Caspase-3.
C Canis familiaris (Dog).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
X NCBI_TaxID=9615;
N [1]
P SEQUENCE FROM N.A.
LA Sano J.;
IT "canine caspase-3 gene.";
IL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
R EMBL; AB085580; BAB92962.1;
R GO; GO:0030693; F:caspase activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR002138; ICE_P10.
R InterPro; IPR001309; ICE_P20.
R InterPro; IPR002398; Peptidase_C14.
R Pfam; PF00656; Peptidase_C14; 1.
R PRINTS; PR00376; ILIBENZYM.
R SMART; SM00115; CASc; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS0207; CASPASE_P10; 1.
R PROSITE; PS0208; CASPASE_P20; 1.
R SEQUENCE 277 AA; 31334 MW; 7094C76D868DAB9 CRC64;
Query Match 20.0%; Score 270.5; DB 6; Length 277;
Best Local Similarity 31.2%; Pred. No. 3.6e-15;
Matches 87; Conservative 40; Mismatches 99; Indels 53; Gaps 11;
Y 4 MESEMSDPLQEEERYDMSGARLALTLCVTK-----AREGSEVDMEALRMFRYL 53
b 27 MDSGMS-----FDNSYKNDYPENGLCIINNNKFNKSTGMAPRSGTVDVAANLRETFTNL 81
Y 54 KFESTMKRDPDTAQOFLEELDFEFOOTIDNWEFVSCAFV-VLMAHGEGLKGEDEKMWLE 112
b 82 KYEVNRKNDLTR-----EILELMSVSKEDHSKRSSFICVLISHDGEGIFGTNGP-VDL 136
Y 113 EDLFEVLNNKNCKALRGKPKVYIIQAQGEHRDPGEELRGNEELGDEELGDEVAVLKNN 172
D Q8MUC3 PRELIMINARY; PRT; 277 AA.
T 01-OCT-2002 (TREMBlrel. 22, Created)
T 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
T 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cysteine protease Cpp32.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
X NCBI_TaxID=9986;
N [1]
P SEQUENCE FROM N.A.
RP MEDLINE=98236830; PubMed=9575916;
RX Wang H.; Keiser J.A.;
RA "Molecular characterization of rabbit Cpp32 and its function in
RT vascular smooth muscle cell apoptosis.";
RL Am. J. Physiol. 274:H1132-H1140(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Wang H.; Keiser J.A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506008; AA47195.1;
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
X Protease.
X SEQUENCE 277 AA; 31653 MW; 7BA4B12E6D43629A CRC64;
Query Match 19.7%; Score 266; DB 6; Length 277;
Best Local Similarity 29.3%; Pred. No. 8.9e-15;
Matches 81; Conservative 45; Mismatches 102; Indels 48; Gaps 10;
Y 6 SEMSDPQLQEEERYDMSGARLALTLCVT-----KAREGSEVDMEALRMFRYLKF 55
b 24 SKMSDCKYLDNSYKNDYPENGLCIINNNKFNKSTGMAPRSGTVDVAANLGETFMNLY 83
Y 56 ESTMKRDPDTAQOFLEELDFEFOOTIDNWEFVSCAFV-VLMAHGEGLKGEDEKMWLE 114
b 84 EYVRNKNDLTR-----EILELMSVSKEDHSKRSSFICVLISHDGEGVYGTNGP-IELKK 138
Y 115 LFEVLNNKNCKALRGKPKVYIIQAQGEHRDPGEELRGNEELGDEELGDEVAVLKNNP 174
b 139 LTSFFRGDYCRSLTGKPKLFIQAQCGTDLDCGIETDSGIB-----TDSGVYDVA--- 184
Y 175 QSITPTVDTLHIYSTVEGYSYRHDKEGSGFTQTLTDV---FIHKKSILELTTEITRLM 231
b 185 QKIPVEADFLYAYSTAPGYYSWRNSKDGSWFQSLCAMLKEYAHK---LEFMHILTRV- 239
Y 232 ANTEVNMQEGK-----PRKVNPEVOSTLRKKLY 258
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Mon Mar 22 14:13:35 2004

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

[1]

SEQUENCE FROM N.A.

TISSUE=Spleen;

Forghani F., Roy S.;

"Rat caspase-7 sequence";

Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

EMBL; AF072124; AAC24011.1; -.

HSSP; P42574; LPAU.

MEROFS; C14.004; -.

GO; GO:0030693; P:caspase activity; IEA.

InterPro; IPR002138; ICE_P10.

InterPro; IPR001309; ICE_P20.

InterPro; IPR002398; Peptidase_C14.

Profam; PF00656; Peptidase_C14; I.

R PRINTS; PRO0376; ILIHCENZYME.

R SMART; SM00115; CASC; 1.

R PROSITE; PS01122; CASPASE_CYS; 1.

R PROSITE; PS01121; CASPASE_HIS; 1.

R PROSITE; PS0207; CASPASE_P10; 1.

R PROSITE; PS0208; CASPASE_P20; 1.

R PROSITE; PS0208; CASPASE_P20; 1.

R PROSITE; PS0208; CASPASE_P20; 1.

R PROSITE; PS0208; CASPASE_P20; 1.

R PROSITE; PS0208; CASPASE_P20; 1.

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R PROSITE; PS0208; CASPASE_P20; 1.

R PROSITE; PS0208; CASPASE_P20; 1.

GenCore version 5.1.1.6
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M protein - protein search, using sw model

run on: March 19, 2004, 11:09:05 ; Search time 10.3586 Seconds
(without alignments)
1306.961 Million cell updates/sec

title: US-09-989-903-2
effect score: 1350
sequence: 1 KPDMESEMSDPOQLQERYD.....KPKKNPEVQSTLRKLYLQ 260

icoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1332	98.7	257	1	ICEE MOUSE
2	940.5	69.7	242	1	ICEE HUMAN
3	290.5	21.5	424	1	ICE2 CHICK
4	276.5	20.5	435	1	ICE2 MOUSE
5	276	20.4	277	1	ICE3 MOUSE
6	274.5	20.3	435	1	ICE2 HUMAN
7	274	20.3	277	1	ICE3 RAT
8	273	20.2	277	1	ICE3 HUMAN
9	263	19.5	277	1	ICE3 CRILLO
10	259.5	19.2	496	1	CEB3 CAEVU
11	257	19.0	416	1	ICE9 HUMAN
12	255.5	18.9	303	1	ICE7 HUMAN
13	254.5	18.9	303	1	ICE7 MOUSE
14	253	18.7	503	1	CEB3 CAREL
15	249.5	18.5	303	1	ICE7 XENLA
16	249.5	18.5	382	1	ICE7 XENLA
17	243	18.0	339	1	ICE DROME
18	242	17.9	480	1	ICE8 HUMAN
19	240.5	17.8	293	1	ICE6 HUMAN
20	235	17.4	276	1	ICE6 MOUSE
21	231.5	17.1	282	1	ICE3 XENLA
22	227.5	16.9	323	1	ICE1 DROME
23	226.5	16.8	299	1	ICE1 SPOR
24	220	16.3	479	1	ICE8 HUMAN
25	219	16.2	312	1	ICE2 RAT
26	217.5	16.1	386	1	ICEA XENLA
27	215.5	16.0	404	1	IIBC HUMAN
28	213	15.8	410	1	IIBC FELCA
29	211	15.6	404	1	IIBC CANFA
30	205	15.2	402	1	IIBC RAT
31	203	15.0	418	1	ICE5 HUMAN
32	201.5	14.9	402	1	IIBC MOUSE
33	200.5	14.9	405	1	IIBC HORSE

34	198.5	14.7	404	1	IIBC PIG
35	198	14.7	521	1	ICEA HUMAN
36	196.5	14.6	419	1	ICEC MOUSE
37	190.5	14.1	377	1	ICE4 HUMAN
38	188.5	14.0	373	1	ICE4 MOUSE
39	175	13.0	377	1	ICED BOVIN
40	112	8.3	484	1	CFLA MOUSE
41	102	7.6	1429	1	NOS1 RAT
42	101.5	7.5	480	1	CFLA HUMAN
43	99	7.3	505	1	ATPA CALSU
44	95.5	7.1	543	1	MVPA DICDI
45	95.5	7.1	580	1	RA50 PYRAB

RESULT 1

ICEE MOUSE

ID ICEE MOUSE STANDARD; PRT; 257 AA.

AC O89094;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mini-ICE) (NICE).

GN CASP14.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC STRAIN=C57BL/6J;

RX MEDLINE=99040667; PubMed=9823333;

RA Ahmad M., Srinivasula S.M., Hegde R., Mukattash R., Fernandes-Alnemri T., Alnemri E.S.;

RT Identification and characterization of murine caspase-14, a new member of the caspase family.";

RL Cancer Res. 58:5201-5205(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Embryo;

RX MEDLINE=99222069; PubMed=10203698;

RA Van de Craen M., Van Loo G., Pyde S., Van Crieckinge W., Van den brande I., Molemans F., Fiers W., Declercq W., Vandenaabeele P.;

RT "Identification of a new caspase homologue: caspase-14.";

RL Cell Death Differ. 5:838-846(1998).

RN [3]

RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.

RX MEDLINE=99009076; PubMed=9792675;

RA Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.;

RT "Caspase-14 is a novel developmentally regulated protease.";

RL J. Biol. Chem. 273:29648-29653(1998).

CC -!- FUNCTION: Seems to be involved in the death receptor and granzyme B apoptotic pathways. May function as a downstream signal transducer of cell death. May play a role in ontogenesis and skin physiology.

CC -!- SUBUNIT: May dimerize with large prodomain caspases.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)

CC -!- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain and kidney.

CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE.

CC -!- SIMILARITY: Belongs to peptidase family C14.

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EMBL; AF092997; AAC63364.1; -
EMBL; AJ007750; CAA07678.1; -
HSP; P29466; 1ICE.
MEROPS; C14.018; -
MGD; MGI:1335092; Casp14.
GO; GO:0006917; P:induction of apoptosis; IDA.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IL1BCENZME.
SMART; SM00115; CASG; 1.
PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Apoptosis; Zymogen.
PROPEP 1 7
CHAIN 8 ?
ACT SITE 93 93
ACT SITE 136 136
MUTAGEN 136 136
SEQUENCE 257 AA; 29458 MW; A228D8DFBAEB84 CRC64;
Query Match 98.7%; Score 1332; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-93;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4 MESEMSDPOPLQEEYDMSGARLALTCVTKAREGSEVDMEALRMFRYLKFTSMKRD 63
1 MSEMSDPOPLQEEYDMSGARLALTCVTKAREGSEVDMEALRMFRYLKFTSMKRD 60
64 TAAQFLLELDEFQOTIDNWEVPSCAFVVLMAHGEGLLKGDEKMWLEDFEVLNKN 123
61 TAAQFLLELDEFQOTIDNWEVPSCAFVVLMAHGEGLLKGDEKMWLEDFEVLNKN 120
124 CKAALRKPKVYIIQACRGHRDPGSELGRNEELGDEGLGDEAVLKNPQSIPTTDT 183
121 CKAALRKPKVYIIQACRGHRDPGSELGRNEELGDEGLGDEAVLKNPQSIPTTDT 180
184 LHYSYVEGLSVRHDEKSGFIQTLTVFHKHGSILELFEETRLMANTENVQEGKPR 243
181 LHYSYVEGLSVRHDEKSGFIQTLTVFHKHGSILELFEETRLMANTENVQEGKPR 240
244 KVNPEVQSTLRKLYLQ 260
241 KVNPEVQSTLRKLYLQ 257

RESULT 2
CEE HUMAN STANDARD; PRT; 242 AA.
D_ICEE HUMAN
C P3194; Q95823;
T 01-JUL-1993 (Rel. 26, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 15-MAR-2004 (Rel. 43, Last annotation update)
E Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
N CASP14.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxId=9606;
N [1]
P SEQUENCE FROM N.A.
C TISSUE=Brain;
X MEDLINE=22158928; PubMed=12181750;
A Pistrutto G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,
Xari C., Lazebnik Y., Rodeck U., Alnemri E.S.;

RT and complex epithelia."
RL Cell Death Differ. 9:995-1006(2002).
RN [2]
RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes."
RL Electrophoresis 13:960-969(1992).
CC -!- FUNCTION: May be involved in the death receptor and granzyme B
apoptotic pathways. May function as a downstream signal transducer
of cell death.
CC -!- SUBUNIT: May dimerize with large prodomain caspases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AF097874; AAD16173.1; -
DR PIR; JC7517; JC7517.
DR HSP; P29466; 1ICE.
DR Aarhus/Ghent-2DPAGE; 6109; IEF.
DR MEROPS; C14.018; -
DR Genew; HGNC:1502; CASP14.
DR MIM; 605848; -
DR GO; GO:0004199; F:caspase activity; TAS.
DR GO; GO:0008544; P:epidermal differentiation; TAS.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 ?
FT CHAIN ? 146
FT CHAIN 147 242
FT ACT SITE 89 89
FT ACT SITE 132 132
FT ACT SITE 132 132
SQ SEQUENCE 242 AA; 27679 MW; E539FB7E8DD808A2 CRC64;
Query Match 69.7%; Score 940.5; DB 1; Length 242;
Best Local Similarity 71.3%; Pred. No. 3.7e-64;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;
8 MSDPQLOEERYDMSGARLALTCVTKAREGSEVDMEALRMFRYLKFTSMKRDPTAQ 67
1 MSNPSLEEEKYDMSGARLALTCVTKAREGSEVDMEALRMFRYLKFTSMKRDPTAQ 60
68 FLELDEFQOTIDNWEVPSCAFVVLMAHGEGLLKGDEKMWLEDFEVLNKNCKAL 127
61 FOLELEKFFQQAIDSDREDFVSCAFVVLMAHGEGLLKGDEKMWLEDFEVLNKNCKAL 120
128 RGKPKVYIIQACRGHRDPGSELGRNEELGDEGLGDEAVLKNPQSIPTTDTLHI 186
121 RAKPKVYIIQACRGHRDPGSELGRNEELGDEGLGDEAVLKNPQSIPTTDTLHV 168
187 YSTVEGYLSYRDEKSGFIQTLTVFHKHGSILELFEETRLMANTENVQEGKPRKN 246
169 YSTVEGYIAYRHEDQKSGFIQTLTVFHKHGSILELFEETRLMANTENVQEGKARTN 228

247 PVQSTLRKLYIQ 260
||:|||||:
229 PRIQSTLRKLYIQ 242

RESULT 3
D ICE2_CHICK STANDARD; PRT; 424 AA.
C Q98943;
I 01-NOV-1997 (Rel. 35, Created)
I 01-NOV-1997 (Rel. 35, Last sequence update)
I 10-OCT-2003 (Rel. 42, Last annotation update)
E Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S)
N CASP2 OR ICH1.
S Gallus gallus (Chicken).
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
C Gallus.
X NCBI_TaxID=9031;
X [1]
P SEQUENCE FROM N.A. (ISOPFORMS ICH-1L AND ICH-1S).
C STRAIN=White leghorn; TISSUE=Ovarian granulosa;
X MEDLINE=97368127; PubMed=9224894;
X Johnson A.L., Brigham J.T., Bergeron L., Yuan J.;
T "Characterization of the avian Ich-1 cDNA and expression of Ich-1L
T mRNA in the hen ovary";
T Gene 192:227-233 (1997).
C -1- FUNCTION: Involved in the activation cascade of caspases
C responsible for apoptosis execution. Might function by either
C activating some proteins required for cell death or inactivating
C proteins necessary for cell survival (By similarity).
C -1- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=2;
C Name=ICH-1L;
C IsoId=Q98943-1; Sequence=Displayed;
C Note=Only form found in the ovary;
C Name=ICH-1S;
C IsoId=Q98943-2; Sequence=VSP_000803, VSP_000804;
C -1- PRT: Heterodimer of a small and a large subunit (By similarity).
C -1- SIMILARITY: Belongs to peptidase family C14.
C -1- SIMILARITY: Contains 1 CARD domain.

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C -----

EMBL; U64963; AAC29881.1; AUT_INIT.
RR HSP; P42574; ICP3.
RR MEROPS; C14.006; -.
RR InterPro; IPR001315; CARD.
RR InterPro; IPR002138; ICE_p10.
RR InterPro; IPR001309; ICE_p20.
RR InterPro; IPR002398; Peptidase_C14.
RR Pfam; PF00619; CARD; 1.
RR Pfam; PF00656; Peptidase_C14; 1.
RR PRINTS; PR00376; ILIBENZYM.
RR SMART; SM00114; CARD; 1.
RR SMART; SM00115; CAS; 1.
RR PROSITE; PS02029; CARD; 1.
RR PROSITE; PS01122; CASPASE_CYS; 1.
RR PROSITE; PS01121; CASPASE_HIS; 1.
RR PROSITE; PS0207; CASPASE_P10; 1.
RR PROSITE; PS0208; CASPASE_P20; 1.
RR Hydroxylase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
PROPEP 1 140
TT CHAIN 141 308 BY SIMILARITY.
TT CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
TT CHAIN 309 424 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).

FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
FT DOMAIN 7 96 CARD.
FT ACT_SITE 248 248 BY SIMILARITY.
FT ACT_SITE 291 291 BY SIMILARITY.
FT VARSPLIC 1 7 Missing (in isoform ICH-1S).
FT VARSPLIC 294 424 /FTID=VSP_000803.
FT DETDRGVQDQKERSDPCCEESDANKENLKLRLPTSD
FT MICYACLGKTAAMRNTKRGSYIEALTTVAEDSDTHVA
FT DMLVKNRQIKQREGVAPGTEFHRCKEMSEYCSLTCRDLYL
FT PGYVPGK -> GVSGIHLPLPCCHCICCSMROTGEWI
FT REMAKNGQIQOAVRVVMTQTKKISSVCVCLHAPI (in
FT isoform ICH-1S).
FT /FTID=VSP_000804.
SQ SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;
Query Match 21.5%; Score 290.5; DB 1; Length 424;
Best Local Similarity 31.0%; Pred. No. 9.3e-15;
Matches 72; Conservative 53; Mismatches 94; Indels 13; Gaps 5;
QY 36 REGSEVDMELERMPYIKFSTMKRDTAQQLLELDEFQQTIDNWEPEVSCAFVVLMA 95
DB 190 RSGDGVDCASLELIFKHLGYQVTFVHDQSAEEMESALERFSKLFDH--QDVDSICVALLS 247
QY 96 HGEELGKGEDEKVRLEDLPEVLNNKNCALRGKPKVYIQACRGSHRDPGBELRGNEE 155
DB 248 HGVGEGVGTOKLQLOEAFRLFDNANCPNLQNKPMPTIQACRGDETDRGVQDQKE 307
QY 156 LG--GDEELGGDEVAVLKNPQSIPTDTLHISTVEGYLSYRHDCKSGFIQITLTV 212
DB 308 RSDSPGCEESDANKENLK--LRLPTRSDMICYACLGKTAAMRNTKRGSYIEALTTV 364
QY 213 FTH--KKSILELEETETRLMANTENVQEGKP---RKVNPEVQSTLRKLYL 259
DB 365 FAEDSRDTHVADMLVKNRQIKQREGVAPGTEFHRCKEMSEYCSLTCRDLYL 416

RESULT 4

ICE2 MOUSE
ID ICE2_MOUSE STANDARD; PRT; 435 AA.
AC R29594; C08737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2
DE protein).
DE CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
RT protein similar to the product of the Caenorhabditis elegans cell
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molemans F., Schotte P., van Criekeinge W., Bayaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69 (1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92328780; PubMed=1378265;
RA Kumar S., Tomooka Y., Noda M.;

I Identification of a set of genes with developmentally down-regulated expression in the mouse brain.";
L Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
C -I- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival. May be important in multistep carcinogenesis.
C -I- SUBUNIT: Heterodimer of a small and a large subunit (By similarity).
C -I- TISSUE SPECIFICITY: High level expression seen in the embryonic CNS, liver, lung, kidney, small intestine, and hair follicles of vibrissae. Moderate expression seen in the skin, oral mucosa, skeletal muscle, submandibular gland and thymus. In the adult, it is highly expressed in spleen, lung and kidney. Moderately in the brain, heart, testis, liver. Low levels in the thymus, skeletal muscle, ovary and gut.
C -I- DEVELOPMENTAL STAGE: During embryonic development is highly expressed in several types of mouse tissue undergoing high rates of programmed cell death such as central nervous system and kidney.
C -I- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT THAT OF OTHER CASPASES (BY SIMILARITY).
C -I- SIMILARITY: Belongs to peptidase family C14.

C -I- SIMILARITY: Contains 1 CARD domain.
C -----
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C -----

R EMBL: D28492; BAA25876.1; ALT INIT.
R EMBL: Y13085; CAA73527.1; ALT_INIT.
R HSSP: P42574; ICP3.

R MEROPS: C14.006; -.
R MGD: MGI:97295; Casp2.

R InterPro: IPR001315; CARD.

R InterPro: IPR002138; ICE_P10.

R InterPro: IPR001309; ICE_P20.

R InterPro: IPR002398; Peptidase_C14.

R Pfam: PF00619; CARD; 1.

R Pfam: PF00656; Peptidase_C14; 1.

R PRINTS: PR00376; ILIBCEZYME.

R SMART: SM00114; CARD; 1.

R SMART: SM00115; CASc; 1.

R PROSITE: PS02029; CARD; 1.

R PROSITE: PS01122; CASPASE_CYS; 1.

R PROSITE: PS01121; CASPASE_HIS; 1.

R PROSITE: PS02027; CASPASE_P10; 1.

R PROSITE: PS02028; CASPASE_P20; 1.

R PROSITE: PS02029; CASPASE_P20; 1.

R Hydroxylase; Thiol protease; Apoptosis; Zymogen.

R PROPEP 1 152 BY SIMILARITY.

R CHAIN 153 316 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).

R CHAIN 317 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).

R CHAIN 331 435 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).

R DOMAIN 15 103 CARD.

R ACT_SITE 260 260 BY SIMILARITY.

R ACT_SITE 303 303 BY SIMILARITY.

R MUTAGEN 303 303 C-XG: LOSS OF FUNCTION.

R CONFLICT 71 71 MISSING (IN REF. 1).

R SEQUENCE 435 AA; 48986 MW; 8984E6AA76E7A676 CRC64;

Query Match 20.58; Score 276.5; DB 1; Length 435;

Best Local Similarity 30.68; Pred. No. 1.1e-13;

Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

36 REGSEVDEALERMFYKPESTMRKQDPTAQOFLDEFTQIDNWEPEVSCAFVILMA 95

202 RSGGDVHTTLVTLFKLLGNVHVDHTAQEQKQLNQFAQ-LPAHRVTDSCV-VALLS 259

QY 96 HGERLLKGEDEKMWLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPG---EELRG 152
DB 260 HGVGGYGVGDGKLLQGVFRFLFDNANCSLQNKMPFIQACRDETDGRVDQDQGN 319
QY 153 NEELGGDEELGGDEVAVLKNPQSIPTDTLHYSTVGYLSYRHDKSGSFIQTLTV 212
DB 320 HTQPGGCEESDAGKEELMK---MRLPTRSDMICGYACLGKNAAMRNTRKGSWYIEALTQV 376
QY 213 FIHKKGSS--ILELTFEITRLWANTVWQEGKP---RKVNPEVQSTLRKKLYL 259
DB 377 FSRACDMHVADMLVKVNLTKEREGYAPGTETFRCKEMSEYCTLCQQLYL 428

RESULT 5

ICE3 MOUSE
ID ICE3 MOUSE STANDARD; PRT; 277 AA.
AC P70677; O08668; Q9QW14;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1) (SCA-1) (LICE).
DE CASP3 OR CPP32.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan I.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme and CED-3.";
RL Oncogene 13:749-755(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224429; PubMed=9070890;
RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and activation of CPP32 in the apoptosis induced by a withdrawal of NGF.";
RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/An;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I., Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scaplehorn M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 A Pahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 A Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 T Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 L [6]
 N SEQUENCE OF 58-277 FROM N.A.
 P Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 A Fortin J.-P., Sekaly R.-P.;
 T "Multiple pathways of apoptosis converging on the CPP32 protease.";
 L Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 C -1- FUNCTION: Involved in the activation cascade of caspases
 C responsible for apoptosis execution. At the onset of apoptosis it
 C proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 C 216-Asp-|-Gly-217 bond. Cleaves and activates sterol regulatory
 C element binding proteins (SREBPs) between the basic helix-loop-
 C helix leucine zipper domain and the membrane attachment domain.
 C Cleaves and activates caspase-6, -7 and -9 (By similarity).
 C Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
 C cytokine which is involved in a variety of inflammatory processes.
 C -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 C (by similarity).
 C -1- SUBCELLULAR LOCATION: Cytoplasmic.
 C -1- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
 C kidney and heart. Lower expression in brain, skeletal muscle and
 C testis.
 C -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 C TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PEPTIDES IS
 C LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 C PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 C CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 C VICE VERSA (BY SIMILARITY).
 C -1- SIMILARITY: Belongs to peptidase family C14.
 C
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 C between the Swiss Institute of Bioinformatics and the EMBL outstation
 C at the European Bioinformatics Institute. There are no restrictions on its
 C use by non-profit institutions as long as its content is in no way
 C modified and this statement is not removed. Usage by and for commercial
 C entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 C or send an email to license@isb-sib.ch).
 C
 C EMBL; U54803; AAC52768.1; -;
 C EMBL; U54802; AAC52768.1; JOINED.
 C EMBL; U49929; AAC52764.1; -;
 C EMBL; D86352; BAA21727.1; -;
 C EMBL; Y13086; CAA73528.1; -;
 C EMBL; U19522; AAC53196.1; -;
 C EMBL; BC038825; AAH38825.2; -;
 C EMBL; U63720; RAD09504.1; -;
 C F1R; JC5410; JCS410.
 C HSP; P42574; IPAU.
 C MEROPS; C14.003; -;
 C MGD; MGI:107739; Casp3.
 C InterPro; IPR002138; ICE_p10.
 C InterPro; IPR001309; ICE_p20.
 C InterPro; IPR002398; Peptidase_C14.
 C Pfam; PF00656; Peptidase_C14; 1.
 C PRINTS; PR00376; ILIBENZYM.
 C SMART; SM00115; CASc; 1.
 C PROSITE; PS01122; CASPASE_CYS; 1.
 C PROSITE; PS01121; CASPASE_HIS; 1.
 C PROSITE; PS02027; CASPASE_P10; 1.
 C PROSITE; PS02028; CASPASE_P20; 1.
 C PROSITE; PS02029; CASPASE_P20; 1.
 C W Hydroxylase; thiol protease; Zymogen; Apoptosis.
 T PROPEP 1 9 BY SIMILARITY.
 T PROPEP 10 28 BY SIMILARITY.
 T CHAIN 29 175 APOPAIN P17 SUBUNIT.

FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT SITE 121 121 BY SIMILARITY.
 FT ACT SITE 163 163 BY SIMILARITY.
 FT CONFLICT 17 17 E -> G (IN REF. 2).
 FT CONFLICT 51 51 N -> T (IN REF. 2).
 FT CONFLICT 63 65 SRS -> ARN (IN REF. 6).
 FT CONFLICT 84 84 Q -> E (IN REF. 2).
 FT CONFLICT 95 95 D -> E (IN REF. 2).
 FT CONFLICT 97 97 L -> M (IN REF. 2).
 FT CONFLICT 128 128 Y -> F (IN REF. 2).
 FT CONFLICT 135 135 E -> D (IN REF. 2).
 FT CONFLICT 231 231 E -> Q (IN REF. 6).
 FT CONFLICT 262 262 I -> F (IN REF. 6).
 SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;
 Query Match 20.4%; Score 276; DB 1; Length 277;
 Best Local Similarity 33.3%; Pred. No. 6.7e-14;
 Matches 79; Conservative 39; Mismatches 81; Indels 38; Gaps 9;
 QY 35 AREGSEVDMEALERNFRVLYKFEETWKRDPDPTAQQLLELDFEQQTIDNWEFVSCAFV-VL 93
 DB 63 SRSGTDVDAANLRFTFMGLKYQVRNKNDLTREDILELMD----SVSKEDHSKSSFCVCI 118
 QY 94 MAHGEGILLKGDGEKQVLEDLFEVLNNKNCALRGPKKVYIIQACRGEHRDPGEELRGN 153
 DB 119 LSHGDEGIYGTNGP-VELKLTSTFFRGDYCESLTGRKPLFIQACRGTELDGIE---- 173
 QY 154 BELGDEELGSGDEVAVLKNNPQSIPYTDTHLHIVSTVEGYLSYRHDKSGSGFTQTLTD-- 211
 DB 174 TDSGTDEENA-----CQKIPVEADFLYASTAPGYYSWRNSKDGSWFIQSLCSML 223
 QY 212 -VFPHKKSILTEITRLMANTVMEQK-----PRKVNPEVQSTLRKKLY 258
 DB 224 KUYAHK-----LEFMILTRV--NRKVATEFESFLDSTFFHAKKQIPCLVSLMLTELY 274
 RESULT 6
 ICE2 HUMAN STANDARD; PRT; 435 AA.
 AC P42575; P42576.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
 DE 11/16).
 GN CASP2 OR ICH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Fetal brain;
 EX MEDLINE=94373811; PubMed=8087842;
 RA Wang L., Maira M., Bergeron L., Zhu H., Yuan J.;
 RT "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
 RT regulators of programmed cell death.";
 RL Cell 78:739-750 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND
 RP GLY-424
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.B., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Deebber A., Martinka S., Maupin R.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP CLEAVAGE SITES.
 RX MEDLINE=96206041; PubMed=8654923;
 RA Xue D., Shahan S., Horvitz H.R.;

"The Caenorhabditis elegans cell-death protein CED-3 is a cysteine protease with substrate specificities similar to those of the human CPP32 protease.";

Genes Dev. 10:1073-1083 (1996).

- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Might function by either activating some proteins required for cell death or inactivating proteins necessary for cell survival.

- SUBUNIT: Heterodimer of a small and a large subunit (By similarity).

- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Comment=Isoforms differ in the N- and C-termini;

Name=ICH-1L;

isoId=p42575-1; Sequence=Displayed;

Notes=Acts as a positive regulator of apoptosis;

Name=ICH-1S;

isoId=p42575-2; Sequence=VSP_000801, VSP_000802;

Notes=Acts as a negative regulator of apoptosis;

- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic lung, liver and kidney than in the heart and brain. In the adults higher level expression is seen in the placenta, lung, kidney, pancreas than in the heart, brain, liver and skeletal muscle.

- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT THAT OF OTHER CASPASES.

- SIMILARITY: Belongs to peptidase family C14.

- SIMILARITY: Contains 1 CARD domain.

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EMBL; U13021; AAA58959.1; -

EMBL; U13022; AAA58960.1; -

EMBL; AY219042; AAO25653.1; -

EMBL; AC073342; AAP22346.1; -

PIR; A54821; A54821.

HSSP; P29466; 1ICE.

MEROPS; C14.006; -

Genew; HGNC:1503; CASP2.

MM; 60639; -

GO; GO:0004202; F.caspase-2 activity; TAS.

GO; GO:0019899; F.enzyme binding; ISS.

GO; GO:0008632; P.apoptotic program; TAS.

GO; GO:0006508; P.proteolysis and peptidolysis; TAS.

InterPro; IPR001315; CARD.

InterPro; IPR002138; ICE_P10.

InterPro; IPR001309; ICE_P20.

InterPro; IPR002398; Peptidase_C14.

Pfam; PF00619; CARD; 1.

Pfam; PF00656; Peptidase_C14; 1.

PRINTS; PR00376; IL1CBENZYME.

SMART; SM00114; CARD; 1.

SMART; SM00115; CASc; 1.

PROSITE; PS50209; CARD; 1.

PROSITE; PS01122; CASPASE_CYS; 1.

PROSITE; PS01121; CASPASE_HIS; 1.

PROSITE; PS50207; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.

Hydrolase; Thiol protease; Apoptosis; Zymogen; Polymorphism; Alternative splicing.

PROPEP 1 152

CHAIN 153 308 CASPASE-2 SUBUNIT P18.

PROPEP 309 316

CHAIN 317 435 CASPASE-2 SUBUNIT P13.

CHAIN 331 435 CASPASE-2 SUBUNIT P12.

DOMAIN 15 103

ACT_SITE 260 260 BY SIMILARITY.

ACT_SITE 303 303 BY SIMILARITY.

FT VARSPLIC 1 14 Missing (in isoform ICH-1S).

FT VARSPLIC 306 435 /FTId=VSP_000801.

FT DETDRVDDGDKNAGSGPGCESDAGKEKLPKMLPTRSD

FT MICGYACLAGTAMNTKSGSVIALAQVFSRACDQHVDA

FT DMLVKVNALIKREGYAPGTEFHRCKEMSEYCSLGRHLYL

FT FGHPTT -> GGAIGSUGHLHLFTAAATASLAL (in

FT isoform ICH-1S).

FT /FTId=VSP_000802.

FT V -> L.

FT /FTId=VAR_016334.

FT P -> A.

FT /FTId=VAR_016335.

FT R -> G.

FT /FTId=VAR_016336.

FT C -> S: LOSS OF FUNCTION.

FT A -> T: LOSS OF FUNCTION.

FT /FTId=VSP_000802.

FT V -> L.

FT /FTId=VAR_016334.

FT P -> A.

FT /FTId=VAR_016335.

FT R -> G.

FT /FTId=VAR_016336.

FT C -> S: LOSS OF FUNCTION.

FT A -> T: LOSS OF FUNCTION.

FT /FTId=VSP_000802.

FT V -> L.

FT /FTId=VAR_016334.

FT P -> A.

FT /FTId=VAR_016335.

FT R -> G.

FT /FTId=VAR_016336.

FT C -> S: LOSS OF FUNCTION.

FT A -> T: LOSS OF FUNCTION.

FT /FTId=VSP_000802.

FT V -> L.

FT /FTId=VAR_016334.

FT P -> A.

FT /FTId=VAR_016335.

RESULT 7

ICE3 RAT

ID ICE3 RAT

AC P5213; P70543; P97699; Q62993;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-NOV-2004 (Rel. 43, Last annotation update)

DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama

DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)

DE (SCA-1) (LICE) (IRP).

GN CASP3 OR CPP32.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxId=10116;

[1]

SEQUENCE FROM N.A.

RP MEDLINE=96358624; PubMed=8761296;

RX Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,

RA Fletcher F.A.;

RT "Molecular characterization of mouse and rat CPP32 beta gene encoding

RT a cysteine protease resembling interleukin-1 beta converting enzyme

RT and CED-3.";

RL Oncogene 13:749-755 (1996).

[2]

RP SEQUENCE OF 30-241 FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=96042508; PubMed=7589240;

RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,

RA Hirshfield A.N., Tilly J.L.;

RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and

RT mammalian cell death: dissociation of IRP-induced oligonucleosomal

RT endonuclease activity from morphological apoptosis in granulosa cells

RT of the ovarian follicle.";

L Endocrinology 136:5042-5053 (1995).

N [3]
P SEQUENCE FROM N.A.

C TISSUE=Brain;

X MEDLINE=97184204; PubMed=9030616;

A Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,

Rostock P. Jr., Poirier G.G., Paul S.M.;

"Cloning and expression of a rat brain interleukin-1beta-converting

enzyme (ICE)-related protease (IRP) and its possible role in

apoptosis of cultured cerebellar granule neurons.";

J. Neurosci. 17:1561-1569 (1997).

L [4]

N SEQUENCE OF 1-264 FROM N.A.

P YAKOVLEV A.G.;

A Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

C -I- FUNCTION: Involved in the activation cascade of caspases

responsible for apoptosis execution. At the onset of apoptosis it

proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a

216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory

element binding proteins (SREBPs) between the basic helix-loop-

helix leucine zipper domain and the membrane attachment domain.

Cleaves and activates caspase-6, -7 and -9 (By similarity).

-I- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit

(By similarity).

-I- SUBCELLULAR LOCATION: Cytoplasmic.

-I- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE

BUT NOT IN KIDNEY OR TESTIS.

-I- DEVELOPMENTAL STAGE: Highly expressed in neuron-enriched regions

of the developing brain, but down-regulated to low levels in the

adult brain.

-I- PTM: CLEAVAGE BY GRANZYME B. CASPASE-6, -8 AND -10 GENERATES THE

TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS

LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED

PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF

CASPASE-7 PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND

VICE VERSA (BY SIMILARITY).

-I- SIMILARITY: Belongs to peptidase family C14.

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EMBL; U49930; AAC52765.1; -

EMBL; U34685; AAC52261.1; -

EMBL; U84410; AAB41792.1; -

EMBL; U58656; AAB02722.1; -

PIR; I67437; I67437.

HSP; P42574; 1PAU.

MEROPS; C14.003; -

InterPro; IPR002138; ICE_p10.

InterPro; IPR001309; ICE_p20.

InterPro; IPR002398; Peptidase_C14.

Pfam; PF00656; Peptidase_C14; 1.

PRINTS; PR00376; ILIBCNZYME.

SMART; SM00115; CASc; 1.

PROSITE; PS01122; CASPASE_CYS; 1.

PROSITE; PS01121; CASPASE_HIS; 1.

PROSITE; PS0207; CASPASE_P10; 1.

PROSITE; PS0208; CASPASE_P20; 1.

Hydrolase; Thiol protease; Zymogen; Apoptosis.

PROPEP 1 9

PROPEP 10 28

CHAIN 29 175

CHAIN 176 277

ACT SITE 121 121

ACT SITE 163 163

CONFLICT 25 29

CONFLICT 170 170

CONFLICT 178 178

T -> A (IN REF. 2).

FT CONFLICT 182 182 M -> V (IN REF. 2).

FT CONFLICT 187 187 I -> K (IN REF. 2).

FT CONFLICT 190 190 E -> G (IN REF. 3).

FT CONFLICT 199 199 T -> S (IN REF. 2).

FT CONFLICT 211 211 L -> G (IN REF. 2).

FT CONFLICT 236 236 D -> I (IN REF. 4).

FT CONFLICT 245 245 T -> M (IN REF. 3).

SQ SEQUENCE 277 AA; 31491 MW; ADABF418E2507402 CRC64;

Query Match 20.3%; Score 274; DB 1; Length 277;

Best Local Similarity 30.5%; Pred. No. 9.5e-14;

Matches 81; Conservative 44; Mismatches 33; Indels 48; Gaps 10;

QY 16 ERYDMSGARLALTLCTV-----KAREGEVDMEALERMFYVKFESTWKRPDPTA 65

Db 34 DSSYKNDYPEMGLCIINNKNFKHSTGNSARNGVDVAANLRRTFMALKYEVNRKNDLTR 93

QY 66 QQFLBELDFEFOQTIDNWEPPVSCAFV-VLMAHGEGLLKGEDEKQVRLDELFEVLNNKNC 124

Db 94 EIMELMD-----SVKEDHSKRSFVGVILSHGDEGVIFGTNGP-VDLKLTFFFRGDYC 148

QY 125 KALRGKPKYIIQACRGEHRDPGELRNEELGGDEELGGDEVAVALKNPQSIPTVTDTL 184

Db 149 RSLTGKPKLFIQACRGTELCGIE-----TDSGTDDMA-----CQKIPVEADFL 194

QY 185 HIYSIVGEVLSYRDEKSGSIOTL---TDVFIHKSGSILELTELTEITELMANTVMOEGK 241

Db 195 YAYSTAPGYISWRNSRDGSGFWIQSLCAKLKYAHK---LEFMILTRV---NRKVATEFE 248

QY 242 -----PRKNPEVQSTLRKKLY 258

Db 249 SPSLDATFHAKKQIPICVSLMTKELY 274

RESULT 8

ICES HUMAN

ID ICE3 HUMAN STANDARD; PRT; 277 AA.

AC P42574; Q96AN1; Q96KE2;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama

protein) (CPP32) (Caspase-3) (SRBHP cleavage activity 1)

DE (SCA-1).

GN CASP3 OR CPP32.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND VARIANT GLU-190.

RC TISSUE=T-cell;

RX MEDLINE=95074098; PubMed=7983002;

RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;

"CPP32, a novel human apoptotic protein with homology to

Cenorhabditis elegans cell death protein Ced-3 and mammalian

interleukin-1 beta-converting enzyme.";

RL J. Biol. Chem. 269:30761-30764 (1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=95292347; PubMed=7774019;

RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,

Baldier D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;

"Xama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable

protease that cleaves the death substrate poly(ADP-ribose)

polymerase.";

RL Cell 81:801-809 (1995).

RN [3]

RP SEQUENCE FROM N.A.

RA Vallette F.M., Oliver L.J.;

"Control of the activation of the procaspase-3 by a sequence located

at the N-terminus of the p17 subunit.";

RT submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RL

[4] SEQUENCE FROM N.A., AND VARIANT GLU-190.

RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RT Schackwitz J.K., Sherwood J.K., Witak L.A., Nickerson D.A.,
RN Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

[5] SEQUENCE FROM N.A., AND VARIANT GLU-190.

RA TISSUE=Lymph;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
A Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
A Scapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Tothyluk S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.B.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length
T human and mouse cDNA sequences";
L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[6] SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.

RA MEDLINE=95319529; PubMed=7596430;
A Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,
A Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
A Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
A Miller D.K.,
T "Identification and inhibition of the ICE/CD-3 protease necessary
T for mammalian apoptosis";
L Nature 376:37-43(1995).

[7] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.

RA MEDLINE=96266352; PubMed=8673606;
A Retonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
A Labelle M., Peterson B.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
A Thornberry N.A., Becker J.W.,
T "The three-dimensional structure of apopain/CPP32, a key mediator of
T apoptosis";
L Nat. Struct. Biol. 3:619-625(1996).

[8] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.

RA MEDLINE=97197830; PubMed=9045680;
A Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
A Priestle J.P., Tomaselli K.J., Gruetter M.G.,
T "Structure of recombinant human CPP32 in complex with the
T tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone";
L J. Biol. Chem. 272:6539-6547(1997).

[9] X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

RA MEDLINE=20283632; PubMed=10821855;
A Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
A Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
A Levy M.D., DeWolfe W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
A Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDewitt P.J.,
A Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
A Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.,
T "Potent and selective nonpeptide inhibitors of caspases 3 and 7
T inhibit apoptosis and maintain cell functionality";
L J. Biol. Chem. 275:16007-16014(2000).

[10] PROCESSED.

RA MEDLINE=96353838; PubMed=8755496;
A Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
KW

RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.,
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).

[11] CLEAVAGE OF HUNTINGTIN.

RA MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vaillancourt J.P., Hayden M.R.,
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract";
RL Nat. Genet. 13:442-449(1996).

CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9. Involved in the
CC cleavage of huntingtin.
CC -!- ENZYME REGULATION: Inhibited by isatin sulfonamides.
CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC and kidney. Moderate levels in brain and skeletal muscle, and low
CC in testis. Also found in many cell lines, highest expression in
CC cells of the immune system.
CC -!- PTM: CLEAVAGE BY GRANTZYME B, APAF-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.

CC -!- SIMILARITY: Belongs to peptidase family C14.

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CC or send an email to license@isb-sib.ch).

EMBL: U13737; AA65015.1; -
EMBL: U13738; AA60355.1; -
EMBL: U26943; AA47429.1; -
EMBL: AJ413269; CAC88866.1; -
EMBL: AY219866; AAO25654.1; -
EMBL: BC016926; AAH16926.1; -
EMBL: PIR; A55315; A55315.
PDB: 1PAU; 07-JUL-97.
PDB: 1CP3; 24-DEC-97.
PDB: 1GFV; 23-JUN-00.
MEROPS: C14.003; -
GeneW: HGNC:1504; CASP3.
MIM: 600636; -
GO: GO:004208; P: caspase-3 activity; TAS.
GO: GO:008624; P: induction of apoptosis by extracellular sig. . . ; TAS.
GO: GO:008629; P: induction of apoptosis by intracellular sig. . . ; TAS.
GO: GO:0009403; P: pathogenesis; TAS.
InterPro: IPR001338; ICE P10.
InterPro: IPR002398; Peptidase C14.
Pfam: PF00656; Peptidase C14; 1.
PRINTS: PR00376; ILIBENZYM.
SMART: SM00115; CASC; 1.
PROSITE: PS01122; CASPASE_CYS; 1.
PROSITE: PS01121; CASPASE_HIS; 1.
PROSITE: PS0207; CASPASE_P10; 1.
PROSITE: PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism.

```
3D-structure. 1 9
PROPEP 10 28
CHAIN 29 175
CHAIN 176 277
ACT SITE 121 121
ACT SITE 163 163
VARIANT 190 190
CONFLICT 31 36
STRAND 36 36
STRAND 43 51
HELIX 57 59
TURN 60 60
TURN 65 65
HELIX 67 80
TURN 81 82

Query Match 20.2%; Score 273; DB 1; Length 277;
Best Local Similarity 31.5%; Pred. No. 1.1e-13;
Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;

6 SEMSDPQLQEEYDMSGARLATLCTVK-----AREGSEVDMEALERMERYLKF 55
24 SEMSDGISLDSNYSKMDYPMGLCIINNNKFNHKTGTSRGTVDVDAANLRETFNLKY 83
56 ESTMKRDPDQAQFLEELDEPQQTIDNWEFPVSCAFV-VLMARHEGLKAGEDEKVRLED 114
84 EVRNKNDLTR----EEIVELMRDVSXEDHSHKRSFVCLLSHGEEGIPTNGP-VDLKK 138
115 LFEVLNKNCKALRGKPKVYIIQACGEHRDCEELRGNEELGGDEELGDEAVLKNKP 174
139 ITNFRGDRCRSLTGKPKLFIQACRGTELDGIE-----TDSGVD-----DMACHK--- 186
175 QSIPTVYDTLHXYSTVEGYSYRHDHSGSGFIQTLTDVFIHKKGSIETELTEITRLMANT 234
187 --IPVDAFLYANSTAPGYYSWRNSKDGWFQSLC-AMLKQYADKLEPMHLTRV--NR 241
235 EVMQEGK-----PRKNPEVQSTLRKLY 258
242 KVATEFESFSDATFFHAKQIQCIVSMLTKELY 274

RESULT 9
ID -ICE3 CRIL0 STANDARD; PRT; 277 AA.
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
DE CASP3 OR CPP32.
DE Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
DE Cricetus.
DE NCBI_TaxID=10030;
DE [1]
DE SEQUENCE FROM N.A.
DE TISSUE=Brain;
DE MEDLINE=96183185; PubMed=8605870;
DE Wang X., Zelenski N.G., Yang J., Sakai J., Brown M.S.,
DE Goldstein J.L.;
DE "Cleavage of sterol regulatory element binding proteins (SREBPs) by
DE CPP32 during apoptosis";
DE EMBO J. 15:1012-1020(1996).
DE -!- FUNCTION: Involved in the activation cascade of caspases
DE responsible for apoptosis execution. At the onset of apoptosis it
DE proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
DE 216-Asp-[Gly-217 bond. Cleaves and activates sterol regulatory
DE element binding proteins (SREBPs) between the basic helix-loop-
```

Caenorhabditis vulgaris.
Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=31233;
[1] _SEQUENCE FROM N.A.
MEDLINE=94061982; PubMed=8242740;
Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
"The C. elegans cell death gene ced-3 encodes a protein similar to
mammalian interleukin-1 beta-converting enzyme.";
Cell 75:641-652(1993).
-!- FUNCTION: Acts as a cysteine protease in controlling programmed
cell death by proteolytically activating or inactivating a
substrate protein or proteins, a potential substrate may be ced-4.
Alternatively it might directly cause cell death by
proteolytically cleaving proteins that are crucial for cell
viability (by similarity).
-!- SUBUNIT: Could be a heterodimer of two subunits derived from the
precursor sequence by a probable autocatalytic mechanism.
-!- PTM: May be regulated by phosphorylation.
-!- SIMILARITY: Belongs to peptidase family C14.
-!- SIMILARITY: Contains 1 CARD domain.
HSPS; P42574; 1CP3.
MEROPS; C14.002;
InterPro; IPR001315; CARD.
InterPro; IPR002138; ICE p10.
InterPro; IPR001309; ICE p20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IL1SCENZYME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
PROSITE; PS02039; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS03037; CASPASE_P10; 1.
PROSITE; PS03038; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
CHAIN 1 364
CELL DEATH PROTEIN 3 SUBUNIT 1
(POTENTIAL).
CHAIN 365 496
CELL DEATH PROTEIN 3 SUBUNIT 2
(POTENTIAL).
CARD.
DOMAIN 1 91
ACT_SITE 308 308 BY SIMILARITY.
ACT_SITE 351 351 BY SIMILARITY.
SEQUENCE 496 AA; 55945 MW; 58E73C790DC3BD38 CRC64;
Query Match 19.2%; Score 259.5; DB 1; Length 496;
Best Local Similarity 29.5%; Pred. No. 2.5e-12;
Matches 70; Conservative 52; Mismatches 96; Indels 19; Gaps 8;
y 36 REGSEVDMALERMFRYLKFEFTMKRDPDPAQOFLBELDFEFOQTDNHEEVSACAFVILMA 95
b 253 RRGTKADKONLNFRCMGY-TVICKDNISGRMLTIRDFAKN----ETHGDSAILVILS 307
y 96 HGEGLGLKDEKMAVLEDFLVLNNKNCALRGKPKVYIIQACRGEHRDPG-----BELR 151
b 308 HGEENVIIQVDDVSVNVNHHIYDILNANAPLANPKLVFVQACKGERDNGFPVLDSVD 367
y 152 GNEEL---GGDEELGDEVAVALKNPQSI-----PYTDLTIYSTVEGYLSYRHKSGS 204
b 368 GVPSLRIRGNDNRDGNFNGVRCPPQAVQVWRKPKSQADILIRYATTAQYVSWRNSARGSW 427
y 205 FICLTLDVFP-IHKKG-SILELTELTEIRLMA-NTEVWQCKPKVNPVEQSTLRKKLY 258
b 428 FIQAVCEVSTHAKDNDVVELLTENVNKKVACGQFISQGANILKQNPETSLRLLKKFY 484
RESULT 11
CE9 HUMAN
D _ICE9 HUMAN STANDARD; Q9BQ62; Q9BQ62; Q9BQ62; Q9BQ62; Q9BQ62;
C P55211; Q95348; Q92852; Q9BQ62; Q9BQ62; Q9BQ62; Q9BQ62; Q9BQ62;
101-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Caspase-9 precursor (EC 3.4.22.2) (CASP-9) (ICE-like apoptotic
protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease
activating factor 3) (APAF-3).
CASP9 OR MCH6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28 AND ARG-221.
RX MEDLINE=96279246; PubMed=8663294;
RA Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,
He W.-W., Dixit V.M.;
"ICE-LAP6, a novel member of the ICS/Ced-3 gene family, is activated
by the cytotoxic T cell protease granzyme B.";
J. Biol. Chem. 271:16720-16724(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PROCESSING.
RC TISSUE=T-cell;
RX MEDLINE=97059171; PubMed=8900201;
RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
Alnemri E.S.;
"The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
mediator CPP32.";
J. Biol. Chem. 271:27099-27106(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=99315341; PubMed=10384055;
RA Hadano S., Nasir J., Nichol K., Rasper D.M., Vaillancourt J.P.,
Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;
"Genomic organization of the human caspase-9 gene on chromosome
1p36.1-p36.3.";
Mamm. Genome 10:757-760(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=99168502; PubMed=10070954;
RA Srinivasula S.M., Ahmad M., Guo Y., Zhan Y., Lazebnik Y.,
Fernandes-Alnemri T., Alnemri E.S.;
"Identification of an endogenous dominant-negative short isoform of
caspase-9 that can regulate apoptosis.";
Cancer Res. 59:999-1002(1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Stomach cancer;
RA Izawa M., Mori T., Ito H., Saitenji T.;
"Molecular cloning and sequencing of a cDNA predicting an alternative
form of pro-caspase-9 from human gastric cancer cell lines.";
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Miho Y., Momoi T., Fujita E.;
"A novel splicing product of human caspase-9 lacking protease
activity.";
Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT VAL-28.
RX MEDLINE=99107856; PubMed=9890966;
RA Seol D.W., Billiar T.R.;
"A caspase-9 variant missing the catalytic site is an endogenous
inhibitor of apoptosis.";
J. Biol. Chem. 274:2072-2076(1999).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28; LEU-99; ILE-102;
VAL-106; ASP-114; HIS-173 AND ARG-221.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
Miyamoto K.E., Nguyen C.P., Nguyen C.P., Poel C.L., Robertson P.D.,
Schackwitz W.S., Sherwood J.K., Witak L.A., Nickerson D.A.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

[9] SEQUENCE FROM N.A. (ISOFORM 1).
A Thomas D.,
L Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
[10]
N SEQUENCE FROM N.A. (ISOFORM 1).
C TISSUE=Eye, and Lymph;
X MEDLINE=22388257; PubMed=12477932;
A Krausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
A Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalak U., Smallos D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
UT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
C -!- FUNCTION: Involved in the activation cascade of caspases
C responsible for apoptosis execution. Binding of caspase-9 to Apaf-
C 1 leads to activation of the protease which then cleaves and
C activates caspase-3. Proteolytically cleaves poly(ADP-ribose)
C polymerase (PARP).
C -!- FUNCTION: Isoform 2 lacks activity is an dominant-negative
C inhibitor of caspase-9.
C -!- SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.
C Caspase-9 and APAF1 bind to each other via their respective NH2-
C terminal CEP-3 homologous domains in the presence of cytochrome C
C and ATP. Interacts with BIRC7.
C -!- ALTERNATIVE PRODUCTS:
C Event=Alternative splicing; Named isoforms=2;
C Name=1; Synonyms=9L, Alpha; displayed;
C IsoId=P5511-1; Sequence=displayed;
C Name=2; Synonyms=9S, Beta;
C IsoId=P5511-2; Sequence=VSP_000818;
C -!- TISSUE SPECIFICITY: Ubiquitous, with highest expression in the
C heart, moderate expression in liver, skeletal muscle, and
C pancreas. Low levels in all other tissues.
C -!- PTM: CLEAVAGES AT ASP-315 BY GRANTZYME B AND AT ASP-330 BY CPP32
C GENERATE THE TWO ACTIVE SUBUNITS. CASPASE-8 AND -10 CAN ALSO BE
C INVOLVED IN THESE PROCESSING EVENTS.
C -!- SIMILARITY: Belongs to peptidase family C14.
C -!- SIMILARITY: Contains 1 CARD domain.
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C or send an email to license@isb-sib.ch).
C
C EMBL; U56390; AAC50640.1; --
C EMBL; U60521; AAC50776.1; --
C EMBL; AB019205; BAA82697.1; --
C EMBL; AB019137; BAA82697.1; JOINED.
C EMBL; AB019198; BAA82697.1; JOINED.
C EMBL; AB019199; BAA82697.1; JOINED.
C EMBL; AB019200; BAA82697.1; JOINED.
C EMBL; AB019201; BAA82697.1; JOINED.
C EMBL; AB019202; BAA82697.1; JOINED.
C EMBL; AB019203; BAA82697.1; JOINED.
C EMBL; AB019204; BAA82697.1; JOINED.
C EMBL; AB019205; BAA82697.1; JOINED.

DR EMBL; AF093130; AAD12248.1; --
DR EMBL; AB015653; BAA78780.1; --
DR EMBL; AB020979; BAA87905.1; --
DR EMBL; AF110376; AAD13615.1; --
DR EMBL; AL512883; CAC42423.1; --
DR EMBL; AY214168; AAO21133.1; --
DR EMBL; BC002452; AAO2452.1; --
DR EMBL; BC006463; AAO06463.1; --
DR PDB; 3YGS; 19-APR-00.
DR MEROPS; C14.010; --
DR Genew; HGNC:1511; CASP9.
DR MIM; 602234; --
DR GO; GO:0004211; F.caspase-9 activity; TAS.
DR GO; GO:0004197; F.cysteine-type endopeptidase activity; TAS.
DR GO; GO:0008047; F.enzyme activator activity; TAS.
DR GO; GO:0008233; F.peptidase activity; TAS.
DR GO; GO:0008632; P.apoptotic program; TAS.
DR GO; GO:0008635; P.caspase activation via cytochrome c; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW Polymorphism; 3D-structure.
FT PROPEP 1 ? POTENTIAL.
FT CHAIN ? 315 CASPASE-9 SUBUNIT P35.
FT PROPEP 316 330 CASPASE-9 SUBUNIT P10.
FT CHAIN 331 416 CARD.
FT DOMAIN 1 92 CARD.
FT ACT_SITE 237 237 BY SIMILARITY.
FT ACT_SITE 287 287 Missing (in isoform 2).
FT VARSPLIC 140 289 /FTId=VSP_000818.
FT VARIANT 28 28 A -> V.
FT VARIANT 99 99 /FTId=VAR_015415.
FT VARIANT 102 102 S -> L.
FT VARIANT 102 102 T -> I (in dbSNP:2308941).
FT VARIANT 106 106 /FTId=VAR_015417.
FT VARIANT 106 106 L -> V (in dbSNP:2308938).
FT VARIANT 114 114 /FTId=VAR_015418.
FT VARIANT 114 114 E -> D (in dbSNP:2020897).
Query Match 19.0%; Score 257; DB 1; Length 416;
Best Local Similarity 29.5%; Pred. No. 3.1e-12;
Matches 75; Conservative 46; Mismatches 89; Indels 44; Gaps 8;
QY 34 KAREGEVMEALERFRKLPKSTWKPQPTAQQLHELDPEQOIIDNWEPEVSCAFVVL 93
Db 178 RTRTGSNIDCEKLRFRFSLHFVMEVKGDLTKAKMVLALLELAQPDHG--ALDCCVVI 234
QY 94 MANGE--GLLKGEDEKVRLEDLFVNLNKNCKALSGKPKVVIQACRGEHRDP 146
Db 235 LSHGCCASHLQFGAVYGTDCGPEVSEKIVNFNGTSCPSLGGKPKLFFIQACGEQKH 294
QY 147 GBEALRGNEELGGDEELGGDEAVLVKNQ--SIPTTDTLHI 186
Db 295 GFEVASTSP--EDESFG--SNPEFDPATFQEGRLTFDQLDAISSLTSPSDFVS 344
QY 187 YSTVEGVLSVRHDEKSGFIOTLTDFVFIHKGSILELTETIRLMANTVMOEGKPKVN 246
Db 345 YSTFPFGVSWRDPKSGSWYVETLLDIF--EQWNSHSDLSILLRVANA-VSKGIYKQW- 400

1 247 BEVQSTLRKGLYLQ 260
2 401 PCGFNPLKRLFFK 414
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RR InterPro; IPR001309; ICE_P20.
RR InterPro; IPR002398; Peptidase_C14.
RR Pfam; PF00656; Peptidase_C14; 1.
RR PRINTS; PR00376; ILIBENZYM.
RR SMART; SMO0115; CASC; 1.
RR PROSITE; PS01122; CASPASE_CYS; 1.
RR PROSITE; PS01121; CASPASE_HIS; 1.
RR PROSITE; PS02027; CASPASE_P10; 1.
RR PROSITE; PS02028; CASPASE_P20; 1.
RR PROSITE; PS02029; CASPASE_P20; 1.
RR Hydroxylase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
RR 3D-structure.
RR PROPEP 1 23
RR CHAIN 24 198
RR PROPEP 199 206
RR CHAIN 207 303
RR ACT_SITE 144 144
RR ACT_SITE 186 186
RR VARSPPLIC 1 1
M -> MDCVGPGRKWHLEKNTSCGSGGICASYVTQM
(in isoform Alpha').
/FTID=VSP 000806.
RR VARSPPLIC 149 303
ELDDGLQADSGPINDTDANPRYKIPVEADFLFAYSTVPGY
SWRSPGRSGFWALCSILEEHGKOLEIMQLTRVNDVAR
HFSQDDHFFHEKQIPCVSNLKELYSQ -> MESCS
VTQAGVQRDLGLTSSPPIPRFQAITRGGAQEEAPGLCPESA
MLIDTRSQWKLTSPPPIPRFQAITRGGAQEEAPGLCPESA
PSWRSTKWTWKSRCSSPG (in isoform Beta).
/FTID=VSP 000807.
RR MUTAGEN 186 186
C-A: NO APOPTOTIC ACTIVITY.
RR CONFLICT 4 4
D -> E (IN REF. 5).
RR CONFLICT 194 194
G -> A (IN REF. 1).
RR SEQUENCE 303 AA; 34276 MW; CD37EB54A232CA4 CRC64;
Query Match 18.9%; Score 255.5; DB 1; Length 303;
Best Local Similarity 30.5%; Pred. No. 2.7e-12;
Matches 80; Conservative 41; Mismatches 100; Indels 41; Gaps 10;
Y 18 RYDMSGARLALTCVTK-----ARGSEVDMEALERFRYKPFSTWKRDPPTA-- 65
b 59 QYNNMFELKGLKIINNKNFDKVTGMVRNGTDKDAEALFKFRSGFVIVYVINDCSAK 118
Y 66 -QQLEELDEFQOTIDNWEFPVSCAFVLMAGEELKGEDEKVMVRLEDLPEVLNNKC 124
b 119 MQDLLKXASEDHT-----NAACFACILLSHGEENVVYGK-GVTPKDLTAHFRGDR 171
Y 125 KALRGKPKYIIQACRGEHDPGEELRGNEELGDEELGDEVAVLKNNPQ-SITYTDT 183
b 172 KTLLEKPLFFIQACRGTELDG-----IQADSGPINDTDA-----NPKYKIPVEAD 219
Y 184 LHIYSTVEGYLSYRHRDKSGFGTQLTDVFIHKKGSILELTEITRL---MANTEWMEG 240
b 220 LPAVSTVPGYYSWSPGRSGFWFQALCSI-LEEHGKDLIMQLIRVNDVARHPESQSD 278
Y 241 KP-----RKVMPEVOSTLRKKLY 258
b 279 DPHEFKKQIPCVVSMLTKEYL 300
RESULT 13
ICE7 MOUSE STANDARD; PRT; 303 AA.
AC P97864; O08669;
JT 01-NOV-1997 (Rel. 35, Created)
JT 01-NOV-1997 (Rel. 35, Last sequence update)
JT 10-OCT-2003 (Rel. 42, Last annotation update)
b Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
b CASP7 OR LICE2.
b Mus musculus (Mouse).
b Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
b Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
b NCBI_TaxID=10090;
b [1]
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RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RL CP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Wortmannin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Lee G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Piers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Atschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Zeehan H., Rubin G.M., Hong L., Scheetz T.B.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalobos D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates sterol
CC regulatory element binding proteins (SREBPs). Overexpression
CC promotes programmed cell death (By similarity).
CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC [1]
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EMBL; U67321; AAC53068.1; ALT_INIT.
EMBL; D66353; BAA19730.1; -
EMBL; Y13088; CAA73530.1; -
EMBL; BC005428; BAH05428.1; -
HSSP; P42574; IPAU.
MEROPS; C14.004; -
MGD; MGI:109383; Casp7.
InterPro; IPR002138; ICE p10.
InterPro; IPR001309; ICE p20.
InterPro; IPR002398; Peptidase C14.
Pfam; PF00656; Peptidase C14; 1.
PRINTS; PR00376; IL1SCENZYM.
SMART; SM00115; CASc; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Apoptosis.
PROPEP 1 23
CHAIN 1 198
PROPEP 199 206
CHAIN 207 303
ACT SITE 144 144
BY SIMILARITY.
CONFLICT 10 11
CONFLICT 45 45
CONFLICT 48 49
SEQUENCE 303 AA; 747787ESBDESF744 CRC64;
Query Match 18.9%; Score 254.5; DB 1; Length 303;
Best Local Similarity 32.5%; Pred. No. 3.2e-12;
Matches 76; Conservative 37; Mismatches 90; Indels 31; Gaps 8;
Y 36 REGSEVDMALRMERYLKFESTMKRDPFA---QQFLELDEFQQTIDNNEEPVSCAFV 92
b 87 RGTGDKAGALFKFONLGFVTVHNDSCAKQDLKRASEEDHSN-----ACFACV 140
Y 93 LMAHGEGLKGEDEKRWLEDLFEYLNKNCALRGPKVYIIQACRGEHRDPGEELRG 152
b 141 LLSHGREDLIYKD-GVTFIKDLTAHFRGDRCKTLEKPKLFFICACRGTELDG----- 194
Y 153 NEELGDEBELGDEVAIVKNNQS-IPVTDPLHYSTVEGYSVHRDEKSGFIQTLTD 211
b 195 -----IQADSGPINDIDANPRNKIPVEADFLFAYSTVPGYSWRNPGKGSWFVQALCS 247
Y 212 VFTHKKGSIETLFTETRL---WANTEVMQEGKPR---KVNPEVQSTLRKKLY 258
b 248 I-LNEHGKOLEIMQILTRYNDRVARHFESQSDPRFNKKQIPCMVSNLTKELY 300
RESULT 14
D -CED3 CABEL STANDARD; PRT; 503 AA.
C P42573; P45435; Q9SQ04; Q9NAQ8;
T 01-NOV-1995 (Rel. 32, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
E Cell death protein 3 precursor (EC 3.4.22.-).
N CED-3 OR C48D1.2.
S Caenorhabditis elegans.
C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
C Rhabditidae; Peloderinae; Caenorhabditis.
X NCBI_TaxID=6239;
X [1]
P SEQUENCE FROM N.A., AND MUTAGENESIS.
C STRAIN=Bristol N2;
X MEDLINE=94061982; PubMed=8242740;
A Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
T "The C. elegans cell death gene ced-3 encodes a protein similar to
T mammalian interleukin-1 beta-converting enzyme.";
L Cell 75:641-652 (1993).
[2]
P REVISION TO 418.
Horvitz H.R.;
Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Burton J.;
Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[4]
REVISIONS.
RA Durbin R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a cysteine protease in controlling programmed
CC cell death by proteolytically activating or inactivating a
CC substrate protein or proteins, a potential substrate may be ced-4.
CC Alternatively it might directly cause cell death by
CC proteolytically cleaving proteins that are crucial for cell
CC viability.
CC -!- SUBUNIT: Could be a heterodimer of two subunits derived from the
CC precursor sequence by a probable autocatalytic mechanism.
CC -!- DEVELOPMENTAL STAGE: Most abundant during embryogenesis and is
CC also detected at later stages.
CC -!- PTM: May be regulated by phosphorylation.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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EMBL; L29052; AAA27982.2; -
EMBL; AF210702; AAG42045.1; -
EMBL; Z81049; CAB61001.2; -
FIR; A49429; A49429.
HSSP; P42574; ICP3.
MEROPS; C14.002; -
WormPep; C48D1.2; CE29088.
InterPro; IPR001315; CARD.
InterPro; IPR002138; ICE p10.
InterPro; IPR001309; ICE p20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IL1SCENZYM.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASc; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
CELL DEATH PROTEIN 3 SUBUNIT 1
CHAIN 1 371
CHAIN 372 503
DOMAIN 1 91
SER-RICH.
BY SIMILARITY.
BY SIMILARITY.
L->F: IN N1040; LOSS OF FUNCTION.
G->R: IN N718; LOSS OF FUNCTION.
G->S: IN N2433; LOSS OF FUNCTION.
A->V: IN N2229/N1164; LOSS OF FUNCTION.
A->V: IN N2430; LOSS OF FUNCTION.
E->K: IN N2426; LOSS OF FUNCTION.
S->F: IN N1163; LOSS OF FUNCTION.
SSQUENCE 503 AA; 56616 MW; 722D5831F94DAA69 CRC64;
Query Match 18.7%; Score 253; DB 1; Length 503;
P REVISION TO 418.

Best Local Similarity 28.9%; Pred. No. 7.9e-12;
Matches 69; Conservative 49; Mismatches 101; Indels 20; Gaps 7;
Y 36 REGSEVDMLEALRMFRYLKFESTMKRDPTAQOFLSEDFQOTIDNWEPPVSCAPVMA 95
b 259 RNETKADKDLNLTNLFRCMGVTYICKNLGTRGMLLTIRDFAK---HESHGDSAILVILS 314
Y 96 HGBEGLLKGEDEKVALEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEELRGNEE 155
b 315 HGBENVIIIGDDTPISTHEIYDILNANPRLANKPKIVFQACGERDNGFFVILDSVD 374
Y 156 -----LGDEBELGG-DEVAVLKNNPQSI-----PTYDTLHIYSTVEGYLSYRHDESKG 202
b 375 GVPAFLRGWDRNDRGLFNLGCVRPQVQWKRKPSQADILAIYATTAQYVWRSNARG 434
Y 203 SGPTQTLTDYF-IHKKG-STLELTERITLMA-NTEVMQEGKPKVNPVQSTLRKKLY 258
b 435 SWFIQAVCEVFSTHAKMDVVELLTENVKVKVACGFTSQSGSNILKQMPBNTSLKKFY 493
RESULT 15
CE7 MESAU
D -ICE7 MESAU STANDARD; PRT; 303 AA.
C P55214;
Y 01-OCT-1996 (Rel. 34, Created)
Y 01-OCT-1996 (Rel. 34, Last sequence update)
Y 28-FEB-2003 (Rel. 41, Last annotation update)
Y Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
Y (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
Y (SCA-2).
Y CASP7 OR MCH3.
Y Mesocricetus auratus (Golden hamster).
Y Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Y Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Y Mesocricetus.
Y NCBI TaxID=10036;
Y [1]
Y SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
Y STRAIN=Syrian; TISSUE=Liver;
Y MEDLINE=96224303; PubMed=8643593;
Y Pai J.-T., Brown M.S., Goldstein J.L.;
Y "Purification and cDNA cloning of a second apoptosis-related cysteine
Y protease that cleaves and activates sterol regulatory element binding
Y proteins.";
Y Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
Y -!- FUNCTION: Involved in the activation cascade of caspases
Y responsible for apoptosis execution. Cleaves and activates sterol
Y regulatory element binding proteins (SREBPs). Proteolytically
Y cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
Y bond. Overexpression promotes programmed cell death (By
Y similarity).
Y -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
Y (By similarity).
Y -!- SUBCELLULAR LOCATION: Cytoplasmic.
Y -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
Y SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
Y CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
Y CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
Y VICE VERSA (BY SIMILARITY).
Y -!- SIMILARITY: Belongs to peptidase family C14.
Y
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Y between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Y or send an email to license@isb-sib.ch).
Y
Y -----
Y EMBL; U47332; AAC52595.1; -.
Y HSSP; P42574; 1PAU.
Y MEROPS; C14.004; -.
Y InterPro; IPR002138; ICE_p10.

DR InterPro: IPR001309; ICE p20.
DR InterPro: IPR002338; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS; PRO0376; ILI1ECZYME.
DR SMART; SM00115; CAS; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;
Query Match 18.5%; Score 249.5; DB 1; Length 303;
Best Local Similarity 32.2%; Pred. No. 7.6e-12;
Matches 76; Conservative 36; Mismatches 89; Indels 35; Gaps 9;
QY 36 REGSEVDMLEALRMFRYLKFESTMKRDPTA---QOFLSEDFQOTIDNWEPPVSCAPV 92
DB 87 RNETKADKDLNLTNLFRCMGVTYICKNLGTRGMLLTIRDFAK---HESHGDSAILV 140
QY 93 LMAHGEGLLKGEDEKVALEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEELRG 152
DB 141 LLSHGSENLTYGKD-GVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTLDGQV--- 196
QY 153 NEELGGDEELGGDEVAVLKNNPQ-SIPTVTDTHIYSTVEGYLSYRHDEKSGFTQTLTD 211
DB 197 -ADSGPINETDA-----NPKYKIPVEADFLFAYSTVPGYYSWNEFGKGSFWFOALCS 247
CY 212 VFTHKGSILELTERITLMAITEVMQEGK-----PRKVNPEVOSTLRKKLY 258
DB 248 I-LDEHGKDLIEIMQLTRV--NDRVARHPESCDDPCFNEKKQIPCMVSMILTKEY 300
Search completed: March 19, 2004, 11:22:45
Job time : 11.3586 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

un on: March 19, 2004, 11:18:31 ; Search time 14.502 Seconds
(without alignments)
1724.577 Million cell updates/sec

file: US-09-989-903-2

effect score: 1350
sequence: 1 KPDSEMSDPPQLQERYD.....KPRKVNPEVQSTLRKLYLQ 260

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues

total number of hits satisfying chosen parameters: 283366

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match %	Length	ID	Description
1	940.5	69.7	242	JC7517	caspase-14/a - hum
2	281	20.8	277	JC5410	CP32 protein - mo
3	274.5	20.3	435	A54821	apoptosis regulato
4	274.5	20.3	452	JC6507	caspase-2 - rat
5	273	20.2	277	A55315	cysteine proteinas
6	268	19.9	454	JC7123	caspase-9 long cha
7	265	19.6	277	S64710	cysteine proteinas
8	255.5	18.9	212	I67437	ICB-LAR6 - human
9	253	18.7	416	G02635	interleukin-1 beta
10	253	18.7	503	A49429	interleukin-1 beta
11	231.5	17.1	495	T20038	hypothetical prote
12	219	16.2	182	I67436	interleukin-1-beta
13	215.5	16.0	311	B56084	interleukin-1-beta
14	215.5	16.0	383	A56084	interleukin-1-beta
15	215.5	16.0	404	A42877	interleukin-1 beta
16	203	15.0	418	B57511	interleukin-1 beta
17	201.5	14.9	402	A46495	IL-1 beta converta
18	200	14.8	312	B54821	apoptosis regulato
19	190.5	14.1	377	A57511	interleukin-1 beta
20	188.5	14.0	263	C56084	interleukin-1-beta
21	186	13.8	826	T43638	caspase-related pr
22	156	11.6	536	T43632	caspase-related pr
23	154	11.4	488	T13385	hypothetical prote
24	147.5	10.9	642	T27021	hypothetical prote
25	142	10.5	136	I53300	interleukin-1-beta
26	102	7.6	1429	S16233	nitric-oxide synth
27	99	7.3	505	S39520	H+-transporting tw
28	97.5	7.2	819	T19351	hypothetical prote
29	96.5	7.1	248	C82376	amino acid ABC tra

30	95.5	7.1	843	2	A47132	major vault protei
31	95.5	7.1	880	2	F75103	conserved hypothet
32	94.5	7.0	1095	2	PC1114	SKDC25 protein -
33	94	7.0	617	2	D56978	hypothetical prote
34	94	7.0	1875	2	S38173	myosin-like protei
35	93.5	6.9	747	2	D95862	probable sensor hi
36	93	6.9	544	2	A42464	microbial metallo
37	92.5	6.9	952	2	D86179	hypothetical prote
38	92.5	6.9	1093	2	A31758	phosphorylase kina
39	92.5	6.9	1093	2	B40793	phosphorylase kina
40	92.5	6.9	1156	2	B70356	chromosome assembl
41	92	6.8	700	2	E69146	sensory transducti
42	91.5	6.8	489	2	S17813	ctdJ protein - Rho
43	91.5	6.8	1920	2	A53188	pericentrin - mous
44	91.5	6.8	2670	2	A46719	inositol 1,4,5-tri
45	91	6.7	971	2	A70179	exodeoxyribonuclea

ALIGNMENTS

RESULT 1

JC7517

caspase-14/a - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7517

R;Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A;Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte

A;Reference number: JC7517; MUID:20517231; PMID:11062009

A;Contents: Epidermal keratinocytes

A;Accession: JC7517

A;Molecule type: mRNA

A;Residues: 1-242 <ECC>

A;Cross-references: GB:AF097874

C;Comment: This enzyme accumulates during keratinocyte differentiation and is activated

C;Genetics:

A;Gene: casp-14/a

A;Map position: 19p13.1

A;Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C;Keywords: differentiation

Query Match 69.7%; Score 940.5; DB 2; Length 242;

Best Local Similarity 71.3%; Pred. No. 2.2e-63;

Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

Qy 8 MSDPQLQERYDMSGARLALILCVTKAREGSEVDMEALERYLYKFESTMKEDPTAQQ 67

Db 1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHNFRQLRFESTMKEDPTAEQ 60

Qy 68 FLEELDEFQOTIDNNEEPVSCAFVVLMAHGEGGLKGEDEKRVRLDELFEVLNNKCKAL 127

Db 61 FQEELEKFOQADSRDPSVCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120

Qy 128 RGKPKYIIQACRGHRDPGEELRGNEELGGDEELGGDE-VAVLKNPQSPITPTDTLHI 186

Db 121 RAKPKYIIQACRGGEORDFG-----ETVGGDEIVVMVKDSQPTPTPTDHLV 169

Qy 187 YSTVEGVLVSRHDEKSGSGFIQTLTVFIHKSGSILELTEEITRLMANTEVMQEGKPKVN 246

Db 169 YSTVEGIYIHRHDKSGSCFIQTLVDVFKRKSHILLELTVETRMVAELVQEGKARKTN 228

Qy 247 PEVQSTLRKLYLQ 260

Db 229 PEIQTSLRKLYLQ 242

RESULT 2

JC5410

CP32 protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999

Accession: J05410
;Species: Homo sapiens (man)
;Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation of apoptosis
;Reference number: J05410; MUID:97224429; PMID:9070890
Accession: J05410
;Status: nucleic acid sequence not shown
Molecule type: mRNA
Residues: 1-277 <NUK>
Cross-references: DDBJ:D86352
Experimental source: embryo
Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 20.8%; Score 281; DB 2; Length 277;
Best Local Similarity 30.8%; Pred. No. 7.6e-14;
Matches 82; Conservative 45; Mismatches 91; Indels 48; Gaps 10;

y 16 ERYDMSGARLALTLCVT-----KAREGSDVMEALERFRLKPESTWKRDPPTA 65
b 34 DSSYKNDYPENGICITIKNPKHSGTGDVDAAANLRFTFMGLKYEVNRKNLDTR 93
y 66 QQLEELDFEQTIDNWEEPVSCAFV-VLMARGEGLLKGEDEKKVRLEDLFVLNNKC 124
b 94 EEIMELMD----SVSKEDHSKSFVCVILSHGDSGVIFGTNGP-VDLKLTSPFRGDYC 148
y 125 KALRGKPVIIOACRGEHRDGEELRGNEELGGDEELGGDEAVLVKNNPOSIFTYTDTL 184
b 149 RSLTGKPLFIIOACRGTGLDCIGIE---TDSGTDEMA-----COKIEVEADFL 194
y 185 HIYSTVEGYLSYRHDEKSGGFQTLLTD---VFHKKGSIILEITRLMANTVMQEGK 241
b 195 YAYSTAPGYYSWNSKDGSWFIOSCLMLKYAHK---LEPMHLIRV--NRKVATEFE 248
y 242 -----PRKNPEVQSILRKLY 258
b 249 SFSLDSTFHAKQIQCIVSMULTKELY 274

RESULT 3
54821
Apoptosis regulator ICH-1, stimulatory form L - human
;Species: Homo sapiens (man)
;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
Accession: A54821
Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
;Title: Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative regulators of apoptosis
;Reference number: A54821; MUID:94373811; PMID:8087842
Accession: A54821
;Status: preliminary
Molecule type: mRNA
Residues: 1-435 <WAN>
Cross-references: GB:U13021; NID:9537291; PID:9537292
Keywords: alternative splicing; apoptosis

Query Match 20.3%; Score 274.5; DB 2; Length 435;
Best Local Similarity 29.7%; Pred. No. 4.1e-13;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;

y 36 REGSVDMEALERFRLKPESTWKRPDTPAQQLFLEELDEFQOTIDNWEPSVSCAFVLM 95
b 202 RSGDVHDHTLTLVTLFKLGYNHVLYDQAQEMQEKLQNAFA-LPAHRVTDSC-IVALLS 259
y 96 HGEBGLKGEDEKVRLEDLFVLNNKCKALKRGPKVYIIQACRGEHRDPG---BELRG 152
b 260 HGVEGAIVGDKLLQLOEVFLFDNANCPSLNQKPKMFFIQACRGETDRGVDDQDGKN 319
y 156 LGGBEELGGDEAVLVKNNPOSIFTYTDTLHIYSTVEGYLSYRHDEKSGGFQTLTDVFI 215
b 320 HAGSPGCESDAGKEKLPKVRILTRSDMICGYACLKGNAMRNTRKGSWTIEALTQV 399
y 216 KKGS--ILEETETRLMANTVMQEGK---RKVNPEVQSILRKLY 259

Accession: J05315
Cysteine protease (EC 3.4.22.-) CPP32 precursor - human
;Alternate names: cysteine proteinase CPP32
;Species: Homo sapiens (man)
;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
Accession: A53315; S58899; I39005
R;Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans C_{ca}-1
;Reference number: A53315; MUID:95074098; PMID:7983002
Accession: A53315
;Status: preliminary
Molecule type: mRNA
Residues: 1-277 <PER>
Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.; Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
;Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian apoptosis
;Reference number: S58899; MUID:95319529; PMID:7596430
Accession: S58899
Molecule type: protein
Residues: 29-46; 176-189, 'E', 191-193 <NIC>
Cell 81, 801-809, 1995
;Title: Yama/CP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease that induces apoptosis
;Reference number: A56924; MUID:95292347; PMID:7774019
Accession: I39005
;Status: preliminary
Molecule type: mRNA
Residues: 1-189, 'E', 191-277 <RES>
Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569

;;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 20.28; Score 273; DB 2; Length 277;
Best Local Similarity 31.58; Pred. No. 3e-13;
Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;
Y 6 SEMSDPQPLQERYDMSGARLATLTCVK-----AREGSEVDMEALRMFRYLKPF 55
Y 24 SEMSDGISLDSNYKMDYPMGLCIINNNKFNHKTGMSRSGTDVDAANLRETFNRLKY 83
Y 56 ESTMKRPTAQQLFELDEFOQTIDNWEPEVSCAFV-VLMHAGEGLLKGDEKVRLED 114
Y 84 EVRNKNDLTR-----EEIVELMRDVSKEHSHKSRFVCLVLSHGEGLIIFGTNGP-VDLKK 138
Y 115 LFEVLNNKCKALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDELGDEAVLKNP 174
Y 139 ITNFRGRDCRSLTGKPKLPIIACRGTLEDGIE-----TDSGVD-----DDMACHK--- 186
Y 175 QSIPTTDTLHIYSTVGYLSYRDEKSGFIQTLDVFIHKKGSILELTHEITRLMANT 234
Y 197 --IPVDADFLYASTAGYYSWRNSKDGWFIOSLC-AMLKQYADKLRFPHILTRV--NR 241
Y 235 EVMQEGK-----PRKVNPEVQSLTKKLY 258
Y 242 KVATEFESFSDATFPAKQIQCIVSMILTKELY 274

RESULT 6

JC7123
Species: long chain - mouse
Species: Mus musculus (house mouse)
Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
Accession: JC7123
Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
Reference number: JC7123; MUID:20001956; PMID:10529400
Accession: JC7123
Status: preliminary
Molecule type: mRNA
Residues: 1-454 <FUD>
Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

Query Match 19.9%; Score 268; DB 2; Length 454;
Best Local Similarity 30.2%; Pred. No. 1.3e-12;
Matches 74; Conservative 45; Mismatches 96; Indels 30; Gaps 8;
Y 36 REGSEVDMEALRMFRYLKPESTMKRDPDTAQQLFELDEFOQTIDNWEPEVSCAFV 95
Y 218 RTGSDNRDKLEHFRMLRFNVEVKNLDTAKQVYALMMAH---RNHRALDCFVVVILS 274
Y 96 HGE-----GLLKGDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPGE 148
Y 275 HGCASHLOFFGAVYGTGCVSVSEKIVNFNGSGCPSLGGKPKLFIQACGGEQKHGF 334
Y 149 ELRGNEELG-----GDEELGGDEAVLKNPQ-----SITYTDTLHIYSTVGYLS 195
Y 335 EVACTSSQGRITLDSSE---PDATFQEGRPRLDQDAVSSLTPSDILVSYSTPFGVS 391
Y 196 YRHDEKSGFIQTLDVFIHKKGSILELTHEITRLMANTVMOEGKPRKVNPEVQSLRK 255
Y 392 WRDKSGSWYIETLDGILFQWARS--EDLQSLLLRVANA-VSEKGYKQI-PCCFNPLRK 447
Y 256 KLYLQ 260
Y 448 KLPFK 452

RESULT 7

564710
Species: Chinese hamster
Species: Cricetulus griseus (Chinese hamster)
Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999

C;Accession: S64710; S72395
R;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
A;Reference number: S64710; MUID:96183185; PMID:8605870
A;Accession: S64710
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-277 <WAW>
A;Cross-references: EMBL:U27463
R;Wang, X.
submitted to the EMBL Data Library, May 1995
A;Reference number: S72395
A;Accession: S72395
A;Molecule type: mRNA
A;Residues: 1-79, 'A', 81-146, 'Y', 148-277 <WAW>
A;Cross-references: EMBL:U27463; NID:91244443; PID:91244444
C;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 19.6%; Score 265; DB 2; Length 277;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
Matches 78; Conservative 35; Mismatches 85; Indels 38; Gaps 9;
Y 36 REGSEVDMEALRMFRYLKPESTMKRDPDTAQQLFELDEFOQTIDNWEPEVSCAFV-VLM 94
Y 64 RSGTDVDAAKLRETFMNLKYEVRNKNLTF-----EEIVELMKNASKEDHSHKSRSFV 119
Y 95 AHGEGLLKGDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPGEELRGNE 154
Y 120 SHGDEGVIFGTGDP-IDLKKLTSYPRGDCRSLGKPKLFIQACRGTLEDGIEHDSGT 178
Y 155 ELGGDEELGGDEAVLKNPQSIPTTDTLHIYSTVGYLSYRDEKSGFIQTLD--- 211
Y 179 E-----DDMTC-----QKIPVADFLYASTAGYYSWRNPKDGSWFIQSLCSMLK 224
Y 212 VFHKKGSILELTHEITRLMANTVMOEGK-----PRKVNPEVOSTLKKLY 258
Y 225 LYAHK-----LEFMHILTRV--NRKVATEFESFSLDSTPEAKQIQCIVSMILTKELY 274

RESULT 8

167437
cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
Accession: 167437
R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirschfield, A.N.; Til
Endocrinology 136, 5042-5053, 1996
Affile: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nuloa cells of the ovarian follicle.
A;Reference number: 153300; MUID:96042508; PMID:7588240
Accession: 167437
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
Residues: 1-212 <RES>
Cross-references: EMBL:U34685; NID:91004370; PID:NAC52261.1; PID:91004371
C;Keywords: cysteine proteinase; hydrolase

Query Match 18.9%; Score 255.5; DB 2; Length 212;
Best Local Similarity 31.4%; Pred. No. 4.5e-12;
Matches 72; Conservative 38; Mismatches 82; Indels 37; Gaps 9;
Y 16 EERDMSGARLATLTCVT-----KARSGSEVDMEALRMFRYLKPESTMKEDPTA 65
Y 5 DSSYKMDYPENGLCIINNNKFNHKTGMSRNGTVDAAANLRETFMALKYVRNKNLDR 64
Y 66 QQFLFELDEFOQTIDNWEPEVSCAFV-VLMHAGEGLLKGDEKVRLEDLFEVLNNKNC 124
Y 65 EEIMELMD-----SVSKEDHSHKSRFVCLVLSHGEGLIIFGTNGP-VDLKKLTSFFRGDYC 119
Y 125 KALRGKPKVYIIQACRGEHRDPGEELRGNEELGGDELGDEAVLKNPQSIPTTDTL 184
Y 120 RSLTGKPKLFIQACRGTLEDGIE-----TDSGAD-----DDVACQKK-----PVEADFL 165

Y 185 HYSTVEGYLVRHDEKSGGPTQTL---TDVFIHKKGSILELTLR 230
b 166 YAYSSAPGYYSWRNRRGGSWFIQSLCAMLKLYAHR---LEFMILTRV 210

RESULT 9

02635

CE-LAP6 - human

;Species: Homo sapiens (man)

;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

;Accession: G02635

;Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,

submitted to the EMBL Data Library, April 1996

;Reference number: H01513

;Accession: G02635

;Status: preliminary; translated from GB/EMBL/DBJ

;Molecule type: mRNA

;Residues: 1-416 <DUA>

;Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027

Query Match 18.7%; Score 253; DB 2; Length 416;

Best Local Similarity 29.1%; Pred. No. 1.6e-11;

Matches 74; Conservative 47; Mismatches 89; Indels 44; Gaps 8;

Y 34 KAREGSEVMEALERNFRYLKFEFTMKRDPDPTAQOFLBELDEFQOTIDNWEFVSCAFVYL 93
b 178 RTRGTGNIDCKLRFRFFSLHFVVEVKGDLTAKKMWLLELRLAQDHG---ALDCCVVVI 234

Y 94 MAGEE-----GLLKGEDEKXVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDP 146

b 235 LSHGCOASHLQFPAGVYGTGCPVSEKIVNIPNGTSCPSUGGKPKLFFIACCGEOKDH 294

Y 147 GSELGRNEELGGDEELGGDEVAVLKNNPQ-----SIPTYDTLHI 186

b 295 GFVASTSP--EDESFG-----SNPEPDATPQEGRLTPDQLDAISSLPTSDIFVS 344

Y 187 YSTVEGYLVRHDEKSGGPTQTLTDVFIHKKGSILELTLRMANTEVMQEGKPKVN 246

b 345 YSTFPFGVSRDPSKGSWYVETLDDIF--EOWAHSEDLQSLLRVANA-VSKGYIKQM- 400

Y 247 PEVQSTLRKKLYQ 260

b 401 PGCFNFIKRLKLPFK 414

RESULT 10

49429

nterleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans

;Species: Caenorhabditis elegans

;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

;Accession: A49429; T37312

;Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.

cell 75, 641-652, 1993

;Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int

;Reference number: A49429; MUID:94061982; PMID:8242740

;Accession: A49429

;Status: preliminary

;Molecule type: DNA

;Residues: 1-503 <YUA>

;Cross-references: GB:L29052; NID:G6503232; PIDN:AAA27982.2; PID:G6503233

;Note: sequence extracted from NCBI backbone (NCBIN:139825; NCBI:P:139826)

;Accession: T37312

;Status: preliminary; translated from GB/EMBL/DBJ

;Molecule type: DNA

;Residues: 1-417, 'R', 419-503 <YU2>

;Cross-references: EMBL:L29052; PIDN:AAA27982.1

;Gene: ced-3

;Genetics:

;Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 18.7%; Score 253; DB 2; Length 503;

Best Local Similarity 28.9%; Pred. No. 2e-11;

Matches 69; Conservative 49; Mismatches 101; Indels 20; Gaps 7;

QY 36 REGSEVMEALERNFRYLKFEFTMKRDPDPTAQOFLBELDEFQOTIDNWEFVSCAFVYLMA 95

Db 259 RGTGKADKXNLNFRMGVYTVICKDNLTGKMLLTIRDFAK---HSHGDSAILVILS 314

QY 96 HGEGLLKGEDEKXVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEBELRGNEE 155

Db 315 HGEENVIIIGVDIPISTHEIYDILLNANAPRLANKPKIVFVQACRGERRDNGFPVLDSVD 374

QY 156 -----LGGDEELGG--DEVAVLKNNPQSI-----PYTDTLHIYSTVEGYLSYRHDEK 202

Db 375 GVPFALRGWNRDGLFNFLGCVRPQVQVWRKPKSQADILLIAYATTAGYVSWRNSARG 434

QY 203 SGFIQTLTDVF--IHKKG--SILELTFEITRLMA--NTEVMQEGKPKVNPEVQSTLRKKLY 258

Db 435 SWFIQAVCEVSTHAKMDVVELLTVNKKVACGFGFQSGSNILKQMPETSLKKFY 493

RESULT 11

T20038

hypothetical protein C48D1.2 - Caenorhabditis elegans

;Species: Caenorhabditis elegans

;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

;Accession: T20038

;Reference number: Z19214

;Status: preliminary; translated from GB/EMBL/DBJ

;Molecule type: DNA

;Residues: 1-435 <WIL>

;Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CBSP:C48D1.2

;Experimental source: clone C48D1

;Genetics:

;A:Gene: CBSP:C48D1.2

;Map position: 4

;A:Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 17.1%; Score 231.5; DB 2; Length 495;

Best Local Similarity 28.3%; Pred. No. 8.1e-10;

Matches 60; Conservative 47; Mismatches 86; Indels 19; Gaps 6;

QY 36 REGSEVMEALERNFRYLKFEFTMKRDPDPTAQOFLBELDEFQOTIDNWEFVSCAFVYLMA 95

Db 258 RGTGKADKXNLNFRMGVYTVICKDNLTGKMLLTIRDFAK---HSHGDSAILVILS 313

QY 96 HGEGLLKGEDEKXVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEBELRGNEE 155

Db 314 HGEENVIIIGVDIPISTHEIYDILLNANAPRLANKPKIVFVQACRGERRDNGFPVLDSVD 373

QY 156 -----LGGDEELGG--DEVAVLKNNPQSI-----PYTDTLHIYSTVEGYLSYRHDEK 202

Db 374 GVPFALRGWNRDGLFNFLGCVRPQVQVWRKPKSQADILLIAYATTAGYVSWRNSARG 433

QY 203 SGFIQTLTDVF--IHKKG--SILELTFEITRLMA 232

Db 434 SWFIQAVCEVSTHAKMDVVELLTVNKKVA 465

RESULT 12

I67436

interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)

;Species: Rattus norvegicus (Norway rat)

;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

;Accession: I67436

;R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirschfield, A.N.; Til

Endocrinology 136: 5042-5053, 1995

;Title: interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel

nuloosa cells of the ovarian follicle.

;Reference number: I53300; MUID:96042508; PMID:7589240

;Accession: I67436

;Status: preliminary; translated from GB/EMBL/DBJ

A:Title: Cloning and expression of four novel isoforms of human interleukin-lbeta conver
A:Reference number: A56084; MUID:95181414; PMID:7876192
A:Accession: A56084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-383 <ALN>
A:Cross-references: GB:U13697; NID:9717039; PIDN:AAC50107.1; PID:9717040
C:Genetics:
A:Gene: IL1BCE
C:Keywords: alternative splicing

Query Match 16.0%; Score 215.5; DB 2; Length 383;
Best Local Similarity 30.3%; Pred. No. 9.3e-09;
Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

QY 22 SGARLALTLCTK-----AREGSEVDMEALERPRYLKFEETMKRDPPTAQQLFLELDEF- 75
DB 139 SRTLALIIICNEEFDSIPRTGAEDVITGMTLLQNLGYSVDVKKNLTASDMTTELEAFA 198
QY 76 ---QOTIDNNEEPVSCAFVYLMAHG-BEGLL-KGEDEK---MVRLEDLFEVLNNKNCKA 126
DB 199 HRPEHKTSDS-----TFLVFMHGIRGICGKHSSEQVPDILQLNAIFNMLNTKNCS 251
QY 127 LRGPVKYIIQACRGEHRDPG-----BELRGNBELGDEBELGDEAVLKNKQPSIPT 179
DB 252 LKDKPKVIIQACRGD--SPGVVWFKDSVGVGNLSLPTTEEFEDD--AIKKAHIEK--- 304
QY 180 YDTLHIYSTVEGYLSYRDEKSGFGIQTLDVFIHKGSILEL-TEETRLMANTENVQ 238
DB 305 --DPIAFCSSTPDNWSRHPTMGVSFVIGRLIE---HMQEVACSDVEIFRKRFSFEQ 359
QY 239 EGKPRKYNPEVQSTLRKKLYL 259
DB 360 DGRAQMPTE-RVTLTRCFYL 379

RESULT 15
A42677
Interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: A54263; A42677; S21734; S24164
R:Cerretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
Genomics 20, 468-473, 1994
A:Title: Molecular characterization of the gene for human interleukin-lbeta converting e
A:Reference number: A54263; MUID:94307734; PMID:8034320
A:Accession: A54263
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-404 <CE2>
A:Cross-references: GB:127475
R:Cerretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
Science 256, 97-100, 1992
A:Title: Molecular cloning of the interleukin-lbeta converting enzyme.
A:Reference number: A42677; MUID:92229430; PMID:1373520
A:Accession: A42677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <CE2>
A:Cross-references: GB:M87507; NID:9435598; PIDN:AAA66942.1; PID:9186286
R:Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.
J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Limjoco, G.; Palyha, O.C.; Raju, S.M.; Rol
Cci, M.J.
Nature 356, 768-774, 1992
A:Title: A novel heterodimeric cysteine protease is required for interleukin-lbeta proce
A:Reference number: S21734; MUID:92244338; PMID:1574116
A:Accession: S21734
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <THO>
A:Cross-references: EMBL:X65019; NID:933792; PIDN:CAA46153.1; PID:933792
R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.;
Arch. Biochem. Biophys. 296, 698-703, 1992

A:Title: Cloning and expression of four novel isoforms of human interleukin-lbeta conver
A:Reference number: A56084; MUID:95181414; PMID:7876192
A:Accession: A56084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-383 <ALN>
A:Cross-references: GB:U13697; NID:9717039; PIDN:AAC50107.1; PID:9717040
C:Genetics:
A:Gene: IL1BCE
C:Keywords: alternative splicing

Query Match 16.2%; Score 219; DB 2; Length 182;
Best Local Similarity 32.1%; Pred. No. 2e-09;
Matches 51; Conservative 39; Mismatches 61; Indels 8; Gaps 4;

QY 36 REGSEVDMEALERPRYLKFEETMKRDPPTAQQLFLELDEFQOTIDNNEEPVSCAFVYLM 95
DB 22 RSGGDVHTTLVTLFPLKLVNHYLYDQAQEMQKQLNPAQ-LPAHRVTDSC-IVALLIS 79
QY 96 HGERGLLKGEDEKVRLEDLFEVLNNKNCKALRGKPVYIIQACRGEHRDPG---BELRG 152
DB 80 HGVGGYGVGDKLQQLQEVFLRFDNANCSLQNKPNFFIQACRGEHTRDGVQDQGN 139
QY 153 NEELGDEBELGDEAVLKNKQPSIPTTYTTLHIYSTVE 191
DB 140 HAQPPGCESDTVKEELMK---MELPTRSDMICVYACLK 175

RESULT 13
A56084
Interleukin-lbeta converting enzyme gamma isozyyme - human
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 05-Nov-1999
A:Accession: B56084
R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A:Title: Cloning and expression of four novel isoforms of human interleukin-lbeta conver
A:Reference number: A56084; MUID:95181414; PMID:7876192
A:Accession: B56084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-311 <ALN>
A:Cross-references: GB:U13698; NID:9717041; PIDN:AAC50108.1; PID:9717042
C:Genetics:
A:Gene: IL1BCE
C:Keywords: alternative splicing

Query Match 16.0%; Score 215.5; DB 2; Length 311;
Best Local Similarity 30.3%; Pred. No. 7.2e-09;
Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

QY 22 SGARLALTLCTK-----AREGSEVDMEALERPRYLKFEETMKRDPPTAQQLFLELDEF- 75
DB 67 SRTLALIIICNEEFDSIPRTGAEDVITGMTLLQNLGYSVDVKKNLTASDMTTELEAFA 126
QY 76 ---QOTIDNNEEPVSCAFVYLMAHG-BEGLL-KGEDEK---MVRLEDLFEVLNNKNCKA 126
DB 127 HRPEHKTSDS-----TFLVFMHGIRGICGKHSSEQVPDILQLNAIFNMLNTKNCS 179
QY 127 LRGPVKYIIQACRGEHRDPG-----BELRGNBELGDEBELGDEAVLKNKQPSIPT 179
DB 180 LKDKPKVIIQACRGD--SPGVVWFKDSVGVGNLSLPTTEEFEDD--AIKKAHIEK--- 232
QY 180 YDTLHIYSTVEGYLSYRDEKSGFGIQTLDVFIHKGSILEL-TEETRLMANTENVQ 238
DB 233 --DPIAFCSSTPDNWSRHPTMGVSFVIGRLIE---HMQEVACSDVEIFRKRFSFEQ 287
QY 239 EGKPRKYNPEVQSTLRKKLYL 259
DB 288 DGRAQMPTE-RVTLTRCFYL 307

RESULT 14
A56084
Interleukin-lbeta converting enzyme beta isozyyme - human
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 05-Nov-1999
A:Accession: A56084
R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995

;Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
;Reference number: S24164; MUID:192337439; PMID:1321594

;Accession: S24164
;Status: preliminary
;Molecule type: protein
;Residues: 120-135,'AX',138-139,'X',141-142 <KRO>
;Genetics:
;Gene: GDB:IL1BC
;Cross-references: GDB:132368; OMIM:147678
;Map position: 11q23-11q23
;Keywords: cysteine proteinase; hydrolase

Query Match 16.0%; Score 215.5; DB 2; Length 404;
Best Local Similarity 30.3%; Pred. No. 1e-08; 96; Indels 43; Gaps 13;
Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;
y 22 SGARLALTLCVTK-----AREGSEVDMEALERMPFLYAKFESTMKEDPTAQOQFLEELDEF- 75
b 160 SRTFLALIIICNEEFDSIPRTGAEDITGMTLLQLNLGYSDVKKNLTASDMTTTELEAFA 219
y 76 ---QOTIDNWEPEVSCAFVLMAG-BEGLL-KGEDEK--MVRLEDLFEVLNNKNCKA 126
b 220 HREHKTSDS-----TLVFMHSHGIRGICGKHSQVDPDILQLNAIFNMLATKNCP 272
y 127 LRCKPKYIIQACRGEHRDPG-----BELRGNBELGGDEELGGDEVAVLKNPQSIPT 179
b 273 LKDKPKVIIQACRGD--SPGVVWFKDSVGVSGNLSLPTTEEFEDD--AIKKAHIEK--- 325
y 180 YDTLAIYSTVEGYLSYRDEKSGFIQTLTDVFIHKKSILEL--TEBITRLMANTVMQ 238
b 326 --DFIAFCSTPDNVSWRHPTWGSVFIGRLIE--HMGEYACSDVEIFRKVFPSEQP 380
y 239 EGKPRKVNPEVQSTLRKKYL 259
b 381 DGRAQMPTE-RVTLTRCFYL 400

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ob time : 15.502 secs

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WM protein - protein search, using sw model

Run on: March 19, 2004, 11:24:16 ; Search time 36.7729 Seconds
(without alignments)

1830.924 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350

Sequence: 1 KPDMESEMSDPPQLOBERYD.....KPKVNPEVQSTLRKLYLQ 260

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgm2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgm2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgm2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgm2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgm2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgm2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgm2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgm2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgm2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgm2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 13: /cgm2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgm2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgm2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgm2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 17: /cgm2_6/ptodata/1/pubaa/US60_NEW_PUBCOMB.pep.*
- 18: /cgm2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	260	9	US-09-989-903-2
2	1350	100.0	260	14	US-10-068-564-2
3	1332	98.7	257	9	US-09-764-803A-2
4	1313	97.3	253	15	US-10-114-432-29
5	968	71.7	185	15	US-10-114-432-35
6	940.5	69.7	242	9	US-09-845-028-2
7	940.5	69.7	242	10	US-09-851-873-105
8	940.5	69.7	242	15	US-10-114-432-3
9	940.5	69.7	242	15	US-10-114-432-15
10	940.5	69.7	242	15	US-10-114-432-17
11	940.5	69.7	242	15	US-10-114-432-18
12	940.5	69.7	242	15	US-10-114-432-26
13	940.5	69.7	242	15	US-10-114-432-27
14	940.5	69.7	242	15	US-10-114-432-28
15	940.5	69.7	242	15	US-10-114-432-30

16	940.5	69.7	242	15	US-10-114-432-31	Sequence 31, Appl
17	940.5	69.7	242	15	US-10-114-432-67	Sequence 67, Appl
18	940.5	69.7	242	15	US-10-114-432-69	Sequence 69, Appl
19	940.5	69.7	242	15	US-10-114-432-71	Sequence 71, Appl
20	940.5	69.7	242	15	US-10-114-432-73	Sequence 73, Appl
21	938.5	69.5	242	15	US-10-114-432-13	Sequence 13, Appl
22	938.5	69.5	242	15	US-10-114-432-23	Sequence 23, Appl
23	935.5	69.3	241	15	US-10-114-432-37	Sequence 37, Appl
24	934.5	69.2	242	9	US-09-989-903-5	Sequence 5, Appl
25	934.5	69.2	242	14	US-10-068-564-5	Sequence 5, Appl
26	928.5	68.8	242	15	US-10-114-432-11	Sequence 11, Appl
27	928.5	68.8	242	15	US-10-114-432-22	Sequence 22, Appl
28	921.5	68.3	241	15	US-10-114-432-36	Sequence 36, Appl
29	921.5	68.3	321	15	US-10-114-432-9	Sequence 9, Appl
30	921.5	68.3	321	15	US-10-114-432-21	Sequence 21, Appl
31	921.5	68.3	321	15	US-10-114-432-66	Sequence 66, Appl
32	921.5	68.3	321	15	US-10-114-432-72	Sequence 72, Appl
33	912.5	67.6	242	9	US-09-764-803A-24	Sequence 24, Appl
34	912.5	67.6	242	9	US-09-845-028-9	Sequence 9, Appl
35	892.5	66.1	229	9	US-09-764-803A-4	Sequence 4, Appl
36	804.5	59.6	214	9	US-09-989-903-9	Sequence 9, Appl
37	804.5	59.6	214	14	US-10-068-564-9	Sequence 34, Appl
38	692.5	51.3	174	15	US-10-114-432-34	Sequence 7, Appl
39	692.5	51.3	230	9	US-09-989-903-7	Sequence 7, Appl
40	692.5	51.3	230	14	US-10-068-564-7	Sequence 5, Appl
41	692.5	51.3	230	15	US-10-114-432-5	Sequence 19, Appl
42	692.5	51.3	230	15	US-10-114-432-19	Sequence 64, Appl
43	692.5	51.3	230	15	US-10-114-432-64	Sequence 68, Appl
44	692.5	51.3	230	15	US-10-114-432-68	Sequence 32, Appl
45	553	41.0	134	15	US-10-114-432-32	

ALIGNMENTS

RESULT 1

US-09-989-903-2
; Sequence 2, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-2

Query Match 100.0%; Score 1350; DB 9; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.3e-122;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KPDMESEMSDPPQLOBERYDMSGARLALTLCTVKAREGSEVDMEALERFRLKPESTMK	60
DB	1	KPDMESEMSDPPQLOBERYDMSGARLALTLCTVKAREGSEVDMEALERFRLKPESTMK	60
QY	61	RDPTAQOFLBELDEFQOTIDNWEPEVSCAFVVLMAHGESGLKGEDEKVRLEDLFEVLN	120
DB	61	RDPTAQOFLBELDEFQOTIDNWEPEVSCAFVVLMAHGESGLKGEDEKVRLEDLFEVLN	120
QY	121	NNCKALRGPKVITQACRGEHRDPGEELGNEELGGDEELGGDEAVLKNPPOSITPY	180
DB	121	NNCKALRGPKVITQACRGEHRDPGEELGNEELGGDEELGGDEAVLKNPPOSITPY	180
QY	181	TDTLHYSTVEGYLSRHDKEGSGFQTTLTDFVFIHKKSILETEITRLMANTVEMQSG	240

b 181 TDTHLYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEG 240
y 241 KPRKVNPEVQSTLRKKLYLQ 260
b 241 KPRKVNPEVQSTLRKKLYLQ 260

RESULT 2
S-10-068-564-2
Sequence 2, Application US/10068564
Publication No. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C2
CURRENT FILING DATE: 2002-02-05
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
S-10-068-564-2

Query Match 100.0%; Score 1350; DB 14; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.3e-122;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 KPDSEMSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMK 60
b 1 KPDSEMSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMK 60
y 61 RDPTAQOFLDEDEFQOTIDNWEPPVSCAFVLMARHGEGLLKGEDEKVRLEDLFEVLN 120
b 61 RDPTAQOFLDEDEFQOTIDNWEPPVSCAFVLMARHGEGLLKGEDEKVRLEDLFEVLN 120
y 121 NKCKALRGKPKVYIIQACRGEHRDPGEELRGNELGGDEKVRLEDLFEVLN 180
b 121 NKCKALRGKPKVYIIQACRGEHRDPGEELRGNELGGDEKVRLEDLFEVLN 180
y 181 TDTHLYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEG 240
b 181 TDTHLYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEG 240
y 241 KPRKVNPEVQSTLRKKLYLQ 260
b 241 KPRKVNPEVQSTLRKKLYLQ 260

RESULT 3
US-09-764-803A-2
Sequence 2, Application US/09764803A
Patent No. US20020034812A1
GENERAL INFORMATION:
APPLICANT: Van de Craen, Marc
APPLICANT: Declercq, Wim
APPLICANT: Vandenabeele, Peter
APPLICANT: Fiers, Walter
TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
FILE REFERENCE: 2676-4661US
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 257

Query Match 97.3%; Score 1313; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 8.5e-119;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMKDPTAQ 67
b 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMKDPTAQ 60
y 68 FLEELDEFQOTIDNWEPPVSCAFVLMARHGEGLLKGEDEKVRLEDLFEVLNKKCAL 127
b 61 FLEELDEFQOTIDNWEPPVSCAFVLMARHGEGLLKGEDEKVRLEDLFEVLNKKCAL 120
y 128 RGKPKVYIIQACRGEHRDPGEELRGNELGGDEKVRLEDLFEVLNKKCAL 187
b 121 RGKPKVYIIQACRGEHRDPGEELRGNELGGDEKVRLEDLFEVLNKKCAL 180
y 188 STVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEGPKVNP 247
b 188 STVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEGPKVNP 247

TYPE: PRT
ORGANISM: Mus musculus
US-09-764-803A-2

Query Match 98.7%; Score 1332; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.2e-120;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MESEMSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMKRDP 63
DB 1 MESEMSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKPFESTMKRDP 60
QY 64 TAQOFLDEDEFQOTIDNWEPPVSCAFVLMARHGEGLLKGEDEKVRLEDLFEVLNKK 123
DB 61 TAQOFLDEDEFQOTIDNWEPPVSCAFVLMARHGEGLLKGEDEKVRLEDLFEVLNKK 120
QY 124 CKALRGKPKVYIIQACRGEHRDPGEELRGNELGGDEKVRLEDLFEVLNKKPQSIPTTDT 183
DB 121 CKALRGKPKVYIIQACRGEHRDPGEELRGNELGGDEKVRLEDLFEVLNKKPQSIPTTDT 180
QY 184 LHIYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEGKPR 243
DB 181 LHIYSTVEGYSYRHDKSGFGIOTLTDVFIHKKGSIILELTHEITRLMANTVWQEGKPR 240
QY 244 KVNPEVQSTLRKKLYLQ 260
DB 241 KVNPEVQSTLRKKLYLQ 257

RESULT 4
US-10-114-432-29
Sequence 29, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Chailita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Ava
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 253
TYPE: PRT
ORGANISM: Mus musculus
US-10-114-432-29

181 STVEGYLSYRDEKSGSFIQTLTDFVFIHKKSILELTSITRLMANTVMOEGKPRKYNP 240
248 EVQSTLRKKLYLQ 260
241 EVQSTLRKKLYLQ 253

RESULT 5
US-10-114-432-35
Sequence 35, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faxis, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovics, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114.432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 185
TYPE: PRT
ORGANISM: Mus musculus
US-10-114-432-35

Query Match 71.7%; Score 968; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.4e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTMKRDPPTAQ 67
Db 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTMKRDPPTAQ 60

2Y 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKNCAL 127
Db 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKNCAL 120

2Y 128 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEAVLKNPNQSIPTTYDTLHI 187
Db 121 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEAVLKNPNQSIPTTYDTLHI 180

2Y 188 STVEG 192
Db 181 STVEG 185

RESULT 6
US-09-845-028-2
Sequence 2, Application US/09845028
Patent No. US20020081705A1
GENERAL INFORMATION:
APPLICANT: Mankovich, John
TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
FILE REFERENCE: BB-111
CURRENT APPLICATION NUMBER: US/09/845.028
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/199,962
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-09-845-028-2

Query Match 69.7%; Score 940.5; DB 9; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

2Y 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTMKRDPPTAQ 67
Db 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTMKRDPPTAQ 60

2Y 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKNCAL 127
Db 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKNCAL 120

2Y 128 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEAVLKNPNQSIPTTYDTLHI 186
Db 121 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEAVLKNPNQSIPTTYDTLHI 168

2Y 187 YSTVEGYLSYRDEKSGSFIQTLTDFVFIHKKSILELTSITRLMANTVMOEGKPRKYN 246
Db 169 YSTVEGYLSYRDEKSGSFIQTLTDFVFIHKKSILELTSITRLMANTVMOEGKPRKYN 228

247 PEVQSTLRKKLYLQ 260
229 PEVQSTLRKKLYLQ 242

RESULT 7
US-09-851-873-105
Sequence 105, Application US/09851873
Publication No. US20030165488A1
GENERAL INFORMATION:
APPLICANT: Kletzien, Rolf F
APPLICANT: Weiland, Katherine L
TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
FILE REFERENCE: 28341/00233
CURRENT APPLICATION NUMBER: US/09/851.873
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-873-105

Query Match 69.7%; Score 940.5; DB 10; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

2Y 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTMKRDPPTAQ 67
Db 1 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFBSTMKRDPPTAQ 60

2Y 68 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKNCAL 127
Db 61 FLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGDEKAVRLDLEFVLNNKNCAL 120

2Y 128 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEAVLKNPNQSIPTTYDTLHI 186
Db 121 RGPKVYIIQACRGEHRDPGEELRGNEELGGDEGLGDEAVLKNPNQSIPTTYDTLHI 168

2Y 187 YSTVEGYLSYRDEKSGSFIQTLTDFVFIHKKSILELTSITRLMANTVMOEGKPRKYN 246
Db 169 YSTVEGYLSYRDEKSGSFIQTLTDFVFIHKKSILELTSITRLMANTVMOEGKPRKYN 228

247 PEVQSTLRKKLYLQ 260
229 PEVQSTLRKKLYLQ 242

RESULT 8
US-10-114-432-3

Sequence 3, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

S-10-114-432-3

Query Match 69.7%; Score 940.5; DB 15; Length 242;

Best Local Similarity 71.3%; Pred. No. 9.7e-83;

Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

```
Y 8 MSDPQLQEEYDMSGARLALTLCTVKAREGSEVDMEALERMFRYLKPESTMKRDPTAQ 67
b 1 MSNPRSEEEKYDMSGARLALTLCTVKAREGSEEDDLAENFRQLRFESTMKRDPTAQ 60
Y 68 FLEELDFQOTIDNWEPEVSCAFVVLMAHGEGLKGEDEKVRLEDFEVNNKNCKAL 127
b 61 FOEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDEKVRLEDFEVNNKNCKAL 120
Y 128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPQSIPTVDTLHI 186
b 121 RAKPKVYIIQACRGEHRDPG-----ETVGGDEIVVMVWIKDSPTIPTVTDALHV 168
Y 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKGSIIELTEETRLMANTENVMOEGKPKVN 246
b 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRKHILLELLETVTRMAEAEVLQEGKARKTN 228
Y 247 PEVOSTLRKLYLQ 260
b 229 PEIQSTLRKLYLQ 242
```

ESULT 9

S-10-114-432-15

Sequence 15, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-114-432-15

Query Match 69.7%; Score 940.5; DB 15; Length 242;

Best Local Similarity 71.3%; Pred. No. 9.7e-83;

Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

```
QY 8 MSDPQLQEEYDMSGARLALTLCTVKAREGSEVDMEALERMFRYLKPESTMKRDPTAQ 67
DB 1 MSNPRSEEEKYDMSGARLALTLCTVKAREGSEEDDLAENFRQLRFESTMKRDPTAQ 60
QY 68 FLEELDFQOTIDNWEPEVSCAFVVLMAHGEGLKGEDEKVRLEDFEVNNKNCKAL 127
DB 61 FOEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDEKVRLEDFEVNNKNCKAL 120
QY 128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPQSIPTVDTLHI 186
DB 121 RAKPKVYIIQACRGEHRDPG-----ETVGGDEIVVMVWIKDSPTIPTVTDALHV 168
QY 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKGSIIELTEETRLMANTENVMOEGKPKVN 246
DB 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRKHILLELLETVTRMAEAEVLQEGKARKTN 228
QY 247 PEVOSTLRKLYLQ 260
DB 229 PEIQSTLRKLYLQ 242
```

RESULT 10

US-10-114-432-17

Sequence 17, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-114-432-17

Query Match 69.7%; Score 940.5; DB 15; Length 242;

Best Local Similarity 71.3%; Pred. No. 9.7e-83;

Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

```
QY 8 MSDPQLQEEYDMSGARLALTLCTVKAREGSEVDMEALERMFRYLKPESTMKRDPTAQ 67
DB 1 MSNPRSEEEKYDMSGARLALTLCTVKAREGSEEDDLAENFRQLRFESTMKRDPTAQ 60
QY 68 FLEELDFQOTIDNWEPEVSCAFVVLMAHGEGLKGEDEKVRLEDFEVNNKNCKAL 127
DB 61 FOEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDEKVRLEDFEVNNKNCKAL 120
QY 128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPQSIPTVDTLHI 186
DB 121 RAKPKVYIIQACRGEHRDPG-----ETVGGDEIVVMVWIKDSPTIPTVTDALHV 168
QY 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKGSIIELTEETRLMANTENVMOEGKPKVN 246
DB 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRKHILLELLETVTRMAEAEVLQEGKARKTN 228
```

247 PEVOSTLRKKLYLQ 260
229 PEIQSTLRKKLYLQ 242

RESULT 11

US-10-114-432-18

Sequence 18, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Faris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-114-432-18

Query Match 69.7%; Score 940.5; DB 15; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

247 8 MSDPQLQEERYDMSGARLALTLCTVKAREGSEVDMEALERMFRYLKFESTMKRDPTAQ 67
229 1 MSNPRSLSEEEKYDMSGARLALTLCTVKAREGSEEDLDALHEMFRLQRFESTMKRDPTAQ 60

68 FLEELDFEFOQTIDNWEPEVSCAFVVLMAHGEGLKGEDEKVRLEDFEVLNNKNCKAL 127
61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDEKVRLEDFEVLNNKNCKAL 120

128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDE-VAVLKNPNQSIPTTYDTLHI 186
121 RAKPKVYIIQACRGEHRDPGEELRGNEELGGDE-VAVLKNPNQSIPTTYDTLHI 168

187 YSTVEGYLSYRHDKSGSGFIQTLTDVFIHKGSILELTFEITRLMANTVMOEGKPKVN 246
169 YSTVEGYIAYRHQDQSGCFIQTLDVFTKRGHILELTFEITRMAEALVQEGKARKTN 228

247 PEVOSTLRKKLYLQ 260
229 PEIQSTLRKKLYLQ 242

RESULT 12

US-10-114-432-26

Sequence 26, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Faris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-26

Query Match 69.7%; Score 940.5; DB 15; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

247 8 MSDPQLQEERYDMSGARLALTLCTVKAREGSEVDMEALERMFRYLKFESTMKRDPTAQ 67
229 1 MSNPRSLSEEEKYDMSGARLALTLCTVKAREGSEEDLDALHEMFRLQRFESTMKRDPTAQ 60

68 FLEELDFEFOQTIDNWEPEVSCAFVVLMAHGEGLKGEDEKVRLEDFEVLNNKNCKAL 127
61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDEKVRLEDFEVLNNKNCKAL 120

128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDE-VAVLKNPNQSIPTTYDTLHI 186
121 RAKPKVYIIQACRGEHRDPGEELRGNEELGGDE-VAVLKNPNQSIPTTYDTLHI 168

187 YSTVEGYLSYRHDKSGSGFIQTLTDVFIHKGSILELTFEITRLMANTVMOEGKPKVN 246
169 YSTVEGYIAYRHQDQSGCFIQTLDVFTKRGHILELTFEITRMAEALVQEGKARKTN 228

247 PEVOSTLRKKLYLQ 260
229 PEIQSTLRKKLYLQ 242

RESULT 13

US-10-114-432-27

Sequence 27, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Bid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Faris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-114-432-27

Query Match 69.7%; Score 940.5; DB 15; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

247 8 MSDPQLQEERYDMSGARLALTLCTVKAREGSEVDMEALERMFRYLKFESTMKRDPTAQ 67
229 1 MSNPRSLSEEEKYDMSGARLALTLCTVKAREGSEEDLDALHEMFRLQRFESTMKRDPTAQ 60

68 FLEELDFEFOQTIDNWEPEVSCAFVVLMAHGEGLKGEDEKVRLEDFEVLNNKNCKAL 127
61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDEKVRLEDFEVLNNKNCKAL 120

128 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDE-VAVLKNPNQSIPTTYDTLHI 186
121 RAKPKVYIIQACRGEHRDPGEELRGNEELGGDE-VAVLKNPNQSIPTTYDTLHI 168

```
b 121 RAKPKYIIQACGEQDPG-----ETVGGDEIYVWIKDSPTIPTYTDALHV 168
y 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKKGSIIELTEETIRLMANTEVWQEGKPRKN 246
b 169 YSTVEGYIAYRHDKSGCFIQLVDVFTKRGHILELLTEVTRMAEAEVQEGKARKTN 228
y 247 PEVQSTLRKLYLQ 260
b 229 PEIQSTLRKLYLQ 242
```

RESULT 14

S-10-114-432-28

Sequence 28, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND

FILE REFERENCE: 51158-20066.00

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 28

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

S-10-114-432-28

```
Query Match 69.7%; Score 940.5; DB 15; Length 242;
Best Local Similarity 71.3%; Pred. No. 9.7e-83;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;
```

```
y 8 MSDPQLQERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKFESTMKRDPTAQ 67
b 1 MSNPRSLSEKXYDMSGARLALTLCVTKAREGSEEDLDLEHMFQRLRFESTMKRDPTAE 60
y 68 FLEELDEFQOTIDNWEPSVSCAFVVLMAHGEGLLKGEDEKMRLEDLFVLLNNKCKAL 127
b 61 FOELEKFXQAIDSDREDPVSCAFVVLMAHGRSGFLKGEDGEMVKLENLFEALNNKCOAL 120
y 128 RGKPKVYIIQACGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPNQSIPTYTDTLHI 186
b 121 RAKPKYIIQACGEQDPG-----ETVGGDSIVMWIKDSPTIPTYTDALHV 168
y 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKKGSIIELTEETIRLMANTEVWQEGKPRKN 246
b 169 YSTVEGYIAYRHDKSGCFIQLVDVFTKRGHILELLTEVTRMAEAEVQEGKARKTN 228
y 247 PEVQSTLRKLYLQ 260
b 229 PEIQSTLRKLYLQ 242
```

RESULT 15

S-10-114-432-30

Sequence 30, Application US/10114432

Publication No. US20040019915A1

GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: March 19, 2004, 11:08:15 ; Search time 52.8287 Seconds

(without alignments)

1390.577 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350

Sequence: 1 KPDMESEMSDPQLQERYD.....KPRKYNPEVQSTLRKKYLYQ 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	281	2	AAW93592 Mouse cas
2	1350	100.0	281	3	AAW93213 Amino aci
3	1332	98.7	257	3	AAW68864 Amino aci
4	940.5	69.7	242	3	AAW93214 Amino aci
5	940.5	69.7	242	5	AAW77980 Full-leng
6	912.5	67.6	242	5	AAW77984 Full-leng
7	892.5	66.1	229	3	AAW68865 Amino aci
8	804.5	59.6	214	3	AAW93216 Amino aci
9	692.5	51.3	230	3	AAW93215 Amino aci
10	436	32.3	398	5	ABG76499 DNA encod
11	427	31.6	234	5	AAU72882 Human asp
12	286.5	21.2	261	4	AAE00610 Chimeric
13	276.5	20.5	452	5	ABW10110 Mouse cas
14	276	20.4	277	4	AAU03395 Mouse cas
15	275.5	20.4	435	2	AAW90703 Interleuk
16	274.5	20.3	435	2	AAW66771 Human int
17	274.5	20.3	435	2	AAW98462 Human ice
18	274.5	20.3	435	2	AAW26274 Cell deat
19	274.5	20.3	435	2	AAW21716 Amino aci
20	274.5	20.3	435	3	ABW14257 Human ich
21	274.5	20.3	435	4	AAE00599 Human cas
22	274.5	20.3	435	5	ABW78321 Human cas
23	274.5	20.3	435	5	ABJ01217 Human cas
24	274.5	20.3	435	7	ADE63002 Human pro
25	274.5	20.3	441	2	AAW66768 Human int

26	274.5	20.3	441	3	ABW14253 Human ich
27	274.5	20.3	452	7	ADB79812 Rat caspa
28	274.5	20.3	452	7	ADE63000 Rat Prote
29	274	20.3	277	2	AAW00372 Apopain C
30	274	20.3	277	2	AAW95831 Human int
31	274	20.3	277	2	AAW00677 Pro-Yama
32	274	20.3	277	2	AAW41688 Amino aci
33	274	20.3	277	2	AAW47089 Rat inter
34	274	20.3	277	6	AAO19867 Bacteriop
35	274	20.3	277	7	ADD25641 Binding d
36	274	20.3	277	7	ADE63080 Rat Prote
37	273	20.2	277	2	AAW16600 Apopain C
38	273	20.2	277	2	AAV21717 Amino aci
39	273	20.2	277	4	AAU05394 Human cas
40	273	20.2	277	4	AAW78712 Pig caspa
41	273	20.2	277	4	AAE00600 Human cas
42	273	20.2	277	5	ABG30904 Human mem
43	273	20.2	277	5	ABJ01218 Human cas
44	273	20.2	277	7	ADE63082 Human pro
45	271	20.1	249	3	AAW26763 Human cas

ALIGNMENTS

RESULT 1

AAW93592

ID AAW93592 standard; protein; 281 AA.

XX AC AAW93592;

XX AC

DT 21-JUN-1999 (first entry)

XX AC

DE Mouse caspase-14 protein.

XX AC

Caspase-14; murine; protease; treatment; apoptotic-related disease; autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS; neurodegenerative disease; ischaemic injury; anti-idiotypic antibody; caspase-14 processing activity; epitope; competitor; modulator.

XX Mus sp.

XX WO9910504-A2.

XX PD 04-MAR-1999.

XX PF 26-AUG-1998; 98WO-US017715.

XX PR 26-AUG-1997; 97US-0056986P.

XX PA (IDUN-) IDUN PHARM INC.

XX PI Alnemri ES, Fernandes-Alnemri T;

XX DR WPI; 1999-204670/17.

XX DR N-PSDB; AAX23515.

Newly isolated polynucleotide encoding a caspase-14 polypeptide - useful for identifying (ant)agonists that are useful in the diagnosis and treatment of apoptosis-related diseases.

XX PS Claim 4; Fig 1; 59pp; English.

This invention describes a novel murine caspase-14 which has protease activity. The caspase-14 polypeptide is useful for identifying (ant)agonists of the polypeptide, where enzyme activity is measured with a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated caspase-14 is useful for identifying inhibitors or enhancers of caspase-14 activity. The compounds identified by both methods form pharmaceutical compositions for treating apoptotic-related diseases, including autoimmune disease, cancer, acquired immunodeficiency syndrome (AIDS), neurodegenerative diseases and ischaemic injury. The anti-caspase-14 antibody is useful for measuring the level of caspase-14 in a tissue

C sample. An antibody that binds to a caspase-14 polypeptide is useful for
 C isolating the polypeptide, and an antibody that binds to the large or
 C small subunit the polypeptide is useful for identifying samples with
 C caspase-14 processing activity. An antibody that binds to caspase-14
 C heterodimer or heterotetramer is useful for isolating caspase-14 with
 C apoptotic activity or in a screening assay to identify (ant)agonists. The
 C antibodies form kits for such purposes. The anti-caspase-14 antibody is
 C also useful for preparing anti-idiotypic antibodies, which mimic a
 C caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
 C the antibody is useful as a competitor of caspase-14 in reducing the
 C level of caspase-14 activity, which reduces the level of apoptotic
 C activity. Oligonucleotides made from the polynucleotides are useful as
 C polymerase chain reaction (PCR) primers or probes to screen genomic or
 C cDNA libraries for similar caspase-14 encoding polynucleotides, or for
 C diagnosis of diseases associated with enhanced or inhibited apoptosis.
 C The isolated caspase-14 gene permits methods of modulating apoptosis for
 C the treatment of human diseases

X X Sequence 281 AA;

Query Match 100.0%; Score 1350; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 5,7e-130;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 KPDMESESDPQLOERYDMSGARLALTLCVTKAREGSEVDMERALMRYLKPESTMK 60
 b 17 KPDMESESDPQLOERYDMSGARLALTLCVTKAREGSEVDMERALMRYLKPESTMK 76
 Y 61 RDPQAQFLLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLN 120
 b 77 RDPQAQFLLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLN 136
 Y 121 NKCKALRGKPKVYIIQACRGEHRDPGELRGNEELGGDEELGGDEAVLKNPQSIPTY 180
 b 137 NKCKALRGKPKVYIIQACRGEHRDPGELRGNEELGGDEELGGDEAVLKNPQSIPTY 196
 Y 181 TDTLHIYSTVEGYLSYRHDKSGFGIQTLDVFIHKKGSIILETTEITRLMANTVMOEG 240
 b 197 TDTLHIYSTVEGYLSYRHDKSGFGIQTLDVFIHKKGSIILETTEITRLMANTVMOEG 256
 Y 241 KPRKNPEVQSTLRKKLYLQ 260
 b 257 KPRKNPEVQSTLRKKLYLQ 276

RESULT 2

AY93213
 ID AAY93213 standard; protein; 281 AA.

AC AAY93213;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a murine caspase-14.

CW Caspase-14; cell death specific protease; apoptosis stimulator;
 OW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

DS Mus sp.

TH Key Location/Qualifiers

FT Region 1..156

FT /note= "large subunit"

FT Active-site 134..138

FT Cleavage-site 156..157

FT Cleavage-site 162..163

FT Region 163..257

FT /note= "small subunit"

PN WO200028047-A1.

OW 18-MAY-2000.

XX

PF 29-OCT-1999; 93WO-US025523.
 XX
 PR 06-NOV-1998; 98US-00187789.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Alnemri ES, Fernandez-Alnemri T;
 XX WPI; 2000-376558/32.
 DR N-PSDB; AAA15163.
 DR

PT Novel nucleic acids encoding cell death specific protease termed caspase-
 PT 14 useful for treating cancers by stimulating apoptosis.

PS Claim 52; Fig 1; 78pp; English.

XX The present sequence represents a murine caspase-14 polypeptide. The
 CC polypeptide is a cell death specific protease, and is an apoptosis
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
 CC -14 antibodies are useful for treating or reducing the severity of
 CC pathological conditions associated with increased or decreased levels of
 CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
 CC diseases and ischemic injury are treated by administering anti-caspase-14
 CC antibodies. The antibody is useful for determining the presence or the
 CC level of caspase-14 in tissue sample and also for the isolation of
 CC caspase-14 with apoptotic activity or in screening assay to identify an
 CC agent that inhibits heterodimer or heterotetramer formation and
 CC therefore, apoptosis

XX Sequence 281 AA;

Query Match 100.0%; Score 1350; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 5,7e-130;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KPDMESESDPQLOERYDMSGARLALTLCVTKAREGSEVDMERALMRYLKPESTMK 60
 Db 17 KPDMESESDPQLOERYDMSGARLALTLCVTKAREGSEVDMERALMRYLKPESTMK 76
 Qy 61 RDPQAQFLLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLN 120
 Db 77 RDPQAQFLLEELDEFQOTIDNWEPEVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLN 136
 Qy 121 NKCKALRGKPKVYIIQACRGEHRDPGELRGNEELGGDEELGGDEAVLKNPQSIPTY 180
 Db 137 NKCKALRGKPKVYIIQACRGEHRDPGELRGNEELGGDEELGGDEAVLKNPQSIPTY 196
 Qy 181 TDTLHIYSTVEGYLSYRHDKSGFGIQTLDVFIHKKGSIILETTEITRLMANTVMOEG 240
 Db 197 TDTLHIYSTVEGYLSYRHDKSGFGIQTLDVFIHKKGSIILETTEITRLMANTVMOEG 256
 Qy 241 KPRKNPEVQSTLRKKLYLQ 260
 Db 257 KPRKNPEVQSTLRKKLYLQ 276

RESULT 3

AY68864

ID AAY68864 standard; protein; 257 AA.

XX AAY68864;

DT 16-MAY-2000 (first entry)

XX Amino acid sequence of a murine caspase-like polypeptide.

DE Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
 XX keratinisation; wound healing.
 KW Mus musculus.

OS WO200004169-A1.

XX

XX

XX

27-JAN-2000.
12-JUL-1999; 99WO-EP004939.
17-JUL-1998; 98EP-00202422.
(VLAAs-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
WPI; 2000-182433/16.
N-PSDB; AAZ60683.
New murine and human caspase homologues useful for treating skin related disorders.
Claim 1; Page 51-52; 68pp; English.
The present sequence represents a murine caspase-like polypeptide. The specification also describes a human caspase-like polypeptide. Caspases are cysteinyl aspartate-specific proteinases which play a central role in apoptosis. The polypeptides of the invention are related to human and murine caspase-2 and human caspase-9, and possess all of the typical amino acids involved in catalysis, including the QACRG box, and contain no or only a very short prodomain. mRNA expression of the homologues of the invention is predominant in the skin. The caspase-like polypeptides are useful for treating human or animal diseases, such as skin diseases. They are also useful for screening for compounds that modulate its activity, i.e. agonists, antagonists, and inhibitors. The caspase-like polypeptides and polynucleotides are useful for modulating keratinisation, for diagnosing and treating inappropriate wound healing

Query Match 98.7%; Score 1332; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.5e-128;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4 MESMSPPQLOEERYDMSGARLALILCVTKAREGSEVDMEALERMFRYLKPESTMKRDP 63
1 MESMSPPQLOEERYDMSGARLALILCVTKAREGSEVDMEALERMFRYLKPESTMKRDP 60
64 TAOQFLEELDEFOOTIDNWEPPVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLNNKN 123
61 TAOQFLEELDEFOOTIDNWEPPVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLNNKN 120
124 CKALRGKPKVITQACRGEHRDPGEELRGNEELGGDEGLGDEAVLKNPQSIPTTDT 183
121 CKALRGKPKVITQACRGEHRDPGEELRGNEELGGDEGLGDEAVLKNPQSIPTTDT 180
184 LHIYSTVEGYLSYRHDKSGFIQTLTDVFIHKKGSILETETITRLMANTVMOEGKPR 243
181 LHIYSTVEGYLSYRHDKSGFIQTLTDVFIHKKGSILETETITRLMANTVMOEGKPR 240
244 KVNFEVOSTLRKKLYLQ 260
241 KVNFEVOSTLRKKLYLQ 257

RESULT 4
LAY93214
ID AAY93214 standard; protein; 242 AA.
AC AAY93214;
XT 04-SEP-2000 (first entry)
DE Amino acid sequence of a human caspase-14.
CW Caspase-14; cell death specific protease; apoptosis stimulator;
GW apoptosis; AIDS; neurodegenerative disease; ischemic injury.
DS Homo sapiens.

XX Key Location/Qualifiers
FH 1. .146
FT /note= "large subunit"
FT 130. .134
FT Active-site
FT 146. .147
FT Cleavage-site
FT 147. .242
FT Region
XX /note= "small subunit"
XX WO200028047-A1.
XX 18-MAY-2000.
XX 23-OCT-1999; 99WO-US025523.
XX 06-NOV-1998; 98US-00187789.
XX (UVEJ-) UNIV JEFFERSON THOMAS.
XX Alnemri ES, Fernandez-Alnemri T;
XX WPI; 2000-376558/32.
XX N-PSDB; AAA15164.
XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
XX Claim 13; Fig 7; 78pp; English.
XX The present sequence represents a human caspase-14 polypeptide. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis

Query Match 69.7%; Score 940.5; DB 3; Length 242;
Best Local Similarity 71.3%; Pred. No. 5.9e-88;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;
8 MSPPQLOEERYDMSGARLALILCVTKAREGSEVDMEALERMFRYLKPESTMKRDP 67
1 MSNPRSELEEKYDMSGARLALILCVTKAREGSEVDMEALERMFRYLKPESTMKRDP 60
68 FLEELDEFOOTIDNWEPPVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLNNKN 127
61 FQBELEKFKQADSDREDPVSCAFVVLMAHGEGLLKGEDEKVRLEDLFEVLNNKN 120
128 RGKPKVITQACRGEHRDPGEELRGNEELGGDEGLGDE-VAVLKNPQSIPTTDT 186
121 RAKPKVITQACRGEHRDPGEELRGNEELGGDEGLGDE-VAVLKNPQSIPTTDT 168
187 YSTVEGYLSYRHDKSGFIQTLTDVFIHKKGSILETETITRLMANTVMOEGKPR 246
169 YSTVEGYLSYRHDKSGFIQTLTDVFIHKKGSILETETITRLMANTVMOEGKPR 228
247 PEVOSTLRKKLYLQ 260
229 PEVOSTLRKKLYLQ 242

RESULT 5
AAG77980
ID AAG77980 standard; protein; 242 AA.
XX

C AAG77980;
X
X
T 05-APR-2002 (first entry)
X Full-length human caspase-14.
X Human; caspase-14; anti-apoptotic; apoptosis.
X Homo sapiens.
S
X WO200181595-A2.
N
X 01-NOV-2001.
D
X 27-APR-2001; 2001WO-US013831.
F
X 27-APR-2000; 2000US-0199962P.
X
X (KNOL) KNOLL GMBH.
A Mankovich JA;
X
X WPI; 2002-041410/05.
R N-PSDB; AAK98248.
X
X Novel isolated human caspase-14 proteins and nucleic acid sequences,
T useful for identifying modulators of caspase-14 protein that are useful
T for modulating apoptosis.
X
X Claim 20; Fig 1; 58pp; English.
S
X The sequence represents the novel full-length human caspase-14 protein,
C referred to as "Caspase-14 NEW" in the specification. The invention
C relates to a novel isolated human caspase-14 protein comprising an amino
C acid sequence with MSNPRSLSE, at its amino terminus. The caspase-14 of
C the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
C of caspase-14 activity. The polypeptide is useful for identifying a
C compound which is a modulator of human caspase-14 activity, and is also
C useful for identifying a compound which modulates the interaction of
C caspase-14 with a target molecule. An antibody to caspase-14 is useful
C for isolating the protein by standard techniques, and for detecting
C caspase-14 to evaluate the abundance and expression pattern. The antibody
C is also useful for diagnostically monitoring protein levels in a tissue
C as a part of a clinical testing procedure. The polypeptide is useful as
C a protease to cleave substrates and for inducing apoptosis in cells, in
C screening assays, and as a bait protein in a two-hybrid or three-hybrid
C assay to identify other proteins that interact with human caspase-14
C protein
X
X Sequence 242 AA;
Q
Query Match 69.7%; Score 940.5; DB 5; Length 242;
Best Local Similarity 71.3%; Pred. No. 5.9e-88;
Matches 18; Conservative 31; Mismatches 29; Indels 13; Gaps 2;
Y 8 MSDFPQIQEERYDMGARGALALTCVTKAREGSEVDMEALERNFRYLKFKSTMKRDPTRAQ 67
b 1 MSNPRSLSEEEKYDMGARGALALTCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTRAQ 60
Y 68 FLEELDEFQOTIOWEPEVSCAFVVLMAHGEGLKGEDEKMKVRLDLEVLNNKNCAL 127
b 61 FQEELEKFAQAIISRDPSVSCAFVVLMAHGRGFLKGEDEKMKVRLDLEVLNNKNCAL 120
Y 128 RGPVKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNKQPSIPTTYDTLHI 186
b 121 RAKPKVYIIQACRGEHRDPG-----ETVGGDEIVMVKDSQTIPTTYTDLHV 168
Y 187 YSTVEGVLVSRHDEKSGFTQTLTDVFIHKKSILELTELTEIRLMANTEVMQEGPKRVN 246
b 169 YSTVEGVIAIRHQQKSGCFIQLVDVTFKRGHILELLTEVTRMAELVQEGKARKTN 228
Y 247 FEVOSTLRKRLYLQ 260
X
X

DB 229 PEIQSTLRKRLYLQ 242
RESULT 6
AAG77984
ID AAG77984 standard; protein; 242 AA.
XX
AC AAG77984;
XX
DT 05-APR-2002 (first entry)
XX
DE Full-length human caspase-14 old.
XX
KW Human; caspase-14; anti-apoptotic; apoptosis.
XX
OS Homo sapiens.
XX
PN WO200181595-A2.
XX
PD 01-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013831.
XX
PR 27-APR-2000; 2000US-0199962P.
XX
PA (KNOL) KNOLL GMBH.
XX
PI Mankovich JA;
XX
DR WPI; 2002-041410/05.
XX
PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.
XX
PS Example; Fig 1; 58pp; English.
XX
CC The sequence represents the full-length human caspase-14 protein,
CC referred to as "Caspase-14 Old" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPRSLSE, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein
XX
SQ Sequence 242 AA;
Query Match 67.6%; Score 912.5; DB 5; Length 242;
Best Local Similarity 71.8%; Pred. No. 4.4e-85;
Matches 176; Conservative 28; Mismatches 28; Indels 13; Gaps 2;
QY 17 EBYDMSGARLALTCVTKAREGSEVDMEALERNFRYLKFKSTMKRDPTRAQFLEELDEFQ 76
Db 10 EKYDMSGARLALTCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTRAQFQELSEKFO 69
QY 77 QTIDNWEPEVSCAFVVLMAHGEGLKGEDEKMKVRLDLEVLNNKNCALRGKPKVYII 136
Db 70 QALDSREDPSVSCAFVVLMAHGRGFLKGEDEKMKVRLDLEVLNNKNCALRAKPKVYII 129
QY 137 QACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNKQPSIPTTYDTLHIYSTVEGVL 195
Db 130 QACRGEHRDPG-----ETVGGDEIVMVKDSQTIPTTYTDLHVYSTVEGIIA 177
X
X

196 YRHDEKSGFIQTLVDVFIHKSGSILELTELTRLMANTVQEGKPRKVNPEVQSTLRK 255
178 YRHDKSGSCFIQTLVDVFTKRKHILELTELTVTRMAELVQEGKARKTNPEIQSTLRK 237
256 KLYLQ 260
238 RLYLQ 242

RESULT 7
AY68865
D AAY68865 standard; protein; 229 AA.
X AAY68865;
T 16-MAY-2000 (first entry)
X Amino acid sequence of a human caspase-like polypeptide.
W Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
W keratinisation; wound healing.
X Homo sapiens.
N WO200004169-A1.
X 27-JAN-2000.
X 12-JUL-1999; 99WO-EP004939.
X 17-JUL-1998; 98EP-00202422.
X (VLAAs) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
X Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
X WPI; 2000-182433/16.
X N-PSDB; AAZ60684.
X New murine and human caspase homologues useful for treating skin related
X disorders.
X Claim 2; Page 53-54; 68pp; English.
X The present sequence represents a human caspase-like polypeptide. The
X specification also describes a murine caspase-like polypeptide. Caspases
X are cysteinyl aspartate-specific proteinases which play a central role in
X apoptosis. The polypeptides of the invention are related to human and
X murine caspase-2 and human caspase-9, and possess all of the typical
X amino acids involved in catalysis, including the QACRG box, and contain
X no or only a very short prodomain. mRNA expression of the homologues of
X the invention is predominant in the skin. The caspase-like polypeptides
X are useful for treating human or animal diseases, such as skin diseases.
X They are also useful for screening for compounds that modulate its
X activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
X polypeptides and polynucleotides are useful for modulating
X keratinisation, for diagnosing and treating inappropriate wound healing

Query Match 66.1%; Score 892.5; DB 3; Length 229;
Best Local Similarity 71.8%; Pred. No. 4.7e-83;
Matches 173; Conservative 27; Mismatches 28; Indels 13; Gaps 2;

21 MSGARLALTLCTVKARGSEVDMEALRMFRYLKPFSTMKGRDPTAQOPLLEDFEFOOTID 80
1 MSGARLALILCTVKARGSEEDLDALEHMFQRFRFSTMKRDPATAFQFOELEKFOQAD 60
81 NWPEFVSCAFVLMAGHEGLLKEGDEKAVRLLEDLFVLNNKNCKALRGKPKVYIIQACR 140
61 SREPFVSCAFVLMAGHEGFLKGEDGEMVKLENLFALNNKNQALRAKPKVYIIQACR 120
141 GEHRDPGEELRGNEELGDEBLGDGE-VAVLVKNPQSIPTTYTDLHIYSTVEGILSYRHD 199

121 GQRDPG-----EVGGDEIVWVKDSQFIPTTYTDLHIYSTVEGILSYRHD 168
200 EKGSGFIQTLVDVFIHKSGSILELTELTRLMANTVQEGKPRKVNPEVQSTLRK 259
169 QKSGCFIQTLVDVFTKRKHILELTELTVTRMAELVQEGKARKTNPEIQSTLRK 228
260 Q 260
229 Q 229

RESULT 8
AAY93216
ID AAY93216 standard; protein; 214 AA.
X AAY93216;
X 04-SBP-2000 (first entry)
X Amino acid sequence of a human caspase-14 splice variant.
X Caspase-14; cell death specific protease; apoptosis stimulator;
X apoptosis; AIDS; neurodegenerative disease; ischemic injury.
X Homo sapiens.
X Key Location/Qualifiers
X Active-site 102..106
X WO200028047-A1.
X 18-MAY-2000.
X 29-OCT-1999; 99WO-US025523.
X 06-NOV-1998; 98US-00187789.
X (UYJE-) UNIV JEFFERSON THOMAS.
X Alnemri ES, Fernandez-Alnemri T;
X WPI; 2000-376558/32.
X N-PSDB; AAA15166.
X Novel nucleic acids encoding cell death specific protease termed caspase-
X 14 useful for treating cancers by stimulating apoptosis.
X Claim 42; Fig 9; 78pp; English.
X The present sequence represents a human caspase-14 splice variant. The
X polypeptide is a cell death specific protease, and is an apoptosis
X stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
X -14 antibodies are useful for treating or reducing the severity of
X pathological conditions associated with increased or decreased levels of
X apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
X diseases and ischemic injury are treated by administering anti-caspase-14
X antibodies. The antibody is useful for determining the presence or the
X level of caspase-14 in tissue sample and also for the isolation of
X caspase-14 with apoptotic activity or in screening assay to identify an
X agent that inhibits heterodimer or heterotetramer formation and
X therefore, apoptosis

Query Match 59.6%; Score 804.5; DB 3; Length 214;
Best Local Similarity 83.0%; Pred. No. 4.7e-74;
Matches 160; Conservative 27; Mismatches 26; Indels 41; Gaps 3;
8 MSQPQLQEBRYDMGARGLALTLCTVKARGSEVDMEALRMFRYLKPFSTMKRDPATQ 67
1 MSNPRSLSEKDYDMGARGLALILCTVKARGSEE----- 34

Y 68 FLEELDEFQOITDINWEEPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLNNKCKAL 127
b 35 --ELEKFKQAIQDSREDPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLNNKCKAL 92
Y 128 RQPKVYIIQACRGEHRDPGEELRGNELGDEELGDE--VAVLKNPQSIPTTDTLHI 186
b 93 RAKPKVYIIQACRGEHRDPGEELRGNELGDEELGDE--VAVLKNPQSIPTTDTLHI 140
Y 187 YSTVEGYLRYHDEKSGFIQTLTDVFIHKKSILLETETRLMANTENVNQGKPKVKN 246
b 141 YSTVEGYIAYRHDKSGFCIQLADVFTKRGHILLETETRLMANTENVNQGKPKVKN 200
Y 247 PEVQSTLRKLYLQ 260
b 201 PEIQSTLRKLYLQ 214

RESULT 9
AY93215
D AAY93215 standard; protein; 230 AA.
X C AAY93215;
X T 04-SEP-2000 (first entry)
X E Amino acid sequence of a human caspase-14 splice variant.
X W Caspase-14; cell death specific protease; apoptosis stimulator;
W apoptosis; AIDS; neurodegenerative disease; ischemic injury.
X S Homo sapiens.
H Key Location/Qualifiers
T Active-site 130..134
X N WO200028047-A1.
D 18-MAY-2000.
X F 29-OCT-1999; 99WO-US025523.
X R 06-NOV-1998; 98US-00187789.
X A (UYJE-) UNIV JEFFERSON THOMAS.
I Alnemri ES, Fernandez-Alnemri T;
R WPI; 2000-376558/32.
R N-PSDB; AAA15165.

Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

Claim 41; Fig 8; 78pp; English.

The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis

Sequence 230 AA;

Query Match 51.3%; Score 692.5; DB 3; Length 230;
Best Local Similarity 72.0%; Pred. NO. 1.7e-62;
Matches 134; Conservative 22; Mismatches 17; Indels 13; Gaps 2;

QY 8 MSDPQLOEERYDMSGARLALTLCVTKAREGSEVDMEALERMERYLKFFSTMKRDPTAQ 67
Db 1 MSNPSLEEEKYDMSGARLALTLCVTKAREGSEVDMEALERMERYLKFFSTMKRDPTAQ 60
QY 68 FLEELDEFQOITDINWEEPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLNNKCKAL 127
Db 61 FOEELKFKQAIQDSREDPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLNNKCKAL 120
QY 128 RQPKVYIIQACRGEHRDPGEELRGNELGDEELGDE--VAVLKNPQSIPTTDTLHI 186
Db 121 RAKPKVYIIQACRGEHRDPGEELRGNELGDEELGDE--VAVLKNPQSIPTTDTLHI 168
QY 187 YSTVEG 192
Db 169 YSTVEG 174

RESULT 10
ABG76499
ID ABG76499 standard; protein; 398 AA.
XX
AC ABG76499;
XX
DT 05-NOV-2002 (first entry)
XX
DE DNA encoding protein modification and maintenance molecule #3.
XX
KW Protein modification and maintenance molecule; gastrointestinal disorder;
KW dysphagia; esophageal spasm; gastritis; anorexia; nausea; hypertension;
KW cardiovascular disorder; atherosclerosis; vasculitis; aneurysm; allergy;
KW ischaemic heart disease; autoimmune disorder; inflammatory disorder;
KW acquired immunodeficiency syndrome; AIDS; ankylosing spondylitis; cancer;
KW anaemia; amyloidosis; cell proliferative; arteriosclerotic bursitis;
KW cirrhosis; developmental disorder; renal tubular acidosis; anaemia;
KW bone resorption; epilepsy; epithelial disorder; keratosis pilaris;
KW allergic contact dermatitis; insect bite; keloid; dermatofibroma; eczema;
KW neurological disorder; stroke; cerebral neoplasm; Alzheimer's disease;
KW Huntington's disease; dementia; reproductive disorder; infertility;
KW endometriosis; gynecomastia; ectopic pregnancy; gene therapy.
XX
OS Homo sapiens.

XX WO200260942-A2.

XX 08-AUG-2002.

XX 30-JAN-2002; 2002WO-US002813.

XX 31-JAN-2001; 2001US-0265705P.

XX 03-FEB-2001; 2001US-0266762P.

XX 16-FEB-2001; 2001US-0269581P.

XX 23-FEB-2001; 2001US-0271198P.

XX 01-MAR-2001; 2001US-0272813P.

XX 13-MAR-2001; 2001US-0275586P.

XX 23-MAR-2001; 2001US-0278505P.

XX 30-MAR-2001; 2001US-0280533P.

XX (INCY-) INCYTE GENOMICS INC.

XX Warren BA, Honchell CD, Lu Y, Wallia NK, Burford N, Delegeane AM;

XX Gandhi AR, Baughn MR, Griffin JA, Gietzen KJ, Lu DAM, Ison CH;

XX Ramkumar J, Tang TY, Lal PG, Borowski ML, Duggan BM, Hafalia AJA;

XX Arviru C, Thangavelu K, Yao MG, Elliott VS, Ding L, Yue H, Lee S;

XX Swarnakar A, Tran UK, Xu Y;

XX WPI; 2002-608499/65.

XX N-PSDB; ABS58370.

New protein modification and maintenance molecules useful for treating or preventing gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, neurological and reproductive disorders.

QY	16	EERVDMGARLALTLCVTK-----ABEGSEVDMEALERWFRFVLKFESTMKEDPTA	65
:	:	:	:
DB	7	DNSYMDYPENGLCIIINNKNFKHKTGTSRGTDDVAANLRTRFNRLKYEVNKDILTR	66
:	:	:	:
QY	66	QQFLLEELDEFQOTIDNWEBPVSFAFV-VLMHAHEEGLLKGEDEKMVRLEDLFVLANKNC	124
:	:	:	:
DB	67	---EEIVELMRDVSKEHDGRSFCVLLSHGEEGIIFCTNGP-VDLAKKITNFRRGDRC	121
:	:	:	:
QY	125	KALRGCKPVYIIIOACRGEHRDPCEELRGNE--ELGGDEELGGDEVAVLKKNPQSIPITYTD	182
:	:	:	:
DB	122	RSLTGPKPLFIIOCRGTETDCGLIETYKTEISEVNLDAPRHDSMACHK-----IPEAD	176
:	:	:	:
QY	183	TLHIYSTVEGYLSYRHDEKSGFTQTLTDFVIHKKSIIULETBEITRLMANTEVMOEKG-	241
:	:	:	:
DB	177	FLYAYSTAPGYYSWRNSKDGSWFTQSLC-AMLQYADKLFFMHILTRV--NRKVATEPES	233
:	:	:	:
QY	242	-----PRKYNFEVOSTLRKKLY	258
:	:	:	:
DB	234	SFDATFHAKKIQCIVSMLTRKELY	258
:	:	:	:
<hr/>			
RESULT 13			
ABB101110			
ID	ABB10110	standard; protein; 452 AA.	
AC	ABB10110;		
XX	DT		
XX	DT		
XX	XX		
DE		Mouse caspase 2 protein.	
XX			
KW		Caspase 2; antisense; cytostatic; osteopathic; cerebroprotective;	
KW		neuroprotective; antilipemic; antiinflammatory; antimicrobial;	
KW		haematopoietic disorder; bone metabolism disorder; cholesterol disorder;	
KW		hyperproliferative disorder; cancer; blood disorder; stroke; inflammation; tumour.	
XX		brain injury; neurodegenerative disease; infection; inflammation; tumour.	
XX			
OS		Mus musculus.	
XX			
PN		WO200224720-A1.	
XX			
PD		28-MAR-2002.	
XX			
PF		14-SEP-2001; 2001WO-US028631.	
XX			
PR		20-SEP-2000; 2000US-00667018.	
XX		(ISIS-) ISIS PHARM INC.	
PA		Zhang H, Watt AT;	
XX			
PI			
XX			
DR		WPI; 2002-351998/38.	
DR		N-PGDB; ABB58563.	
XX			
PT		New antisense compounds targeted to nucleic acid molecule encoding	
PT		caspase 2, useful for treating diseases or conditions associated with	
PT		caspase 2, e.g. cancer, blood disorders, stroke, brain injury and	
PT		neurodegenerative diseases.	
XX			
XX			
PS		Example 13; Page 111-113; 146pp; English.	
XX			
CC		The invention relates to a compound 8-50 nucleobases in length targeted	
CC		to a nucleic acid molecule encoding caspase 2, which specifically	
CC		hybridises with and inhibits the expression of caspase 2, or specifically	
CC		hybridises with at least an 8-nucleobase portion of an active site on a	
CC		nucleic acid molecule encoding caspase 2. The activity of antisense	
CC		oligonucleotides of the invention may be described as, cytostatic,	
CC		osteopathic, cerebroprotective, neuroprotective, antilipemic, useful	
CC		antiinflammatory and antimicrobial. The antisense compounds are useful	
CC		for treating an animal having a disease or condition associated with	
CC		caspase 2, such as haematopoietic disorder, bone metabolism disorder,	
CC		cholesterol disorder, or a hyperproliferative disorder. These compounds	
CC		further be used as research reagents and diagnostics, to distinguish	
CC		mav further be used as research reagents and diagnostics, to distinguish	

c tissue homeostasis, to overcome viral infections and to treat
c immunosuppression-related disorders

x Sequence 435 AA;
2 Query Match 20.4%; Score 275.5; DB 2; Length 435;
Best Local Similarity 29.6%; Pred. No. 3.4e-19;
Matches 68; Conservative 53; Mismatches 100; Indels 9; Gaps 4;
y 36 RGSSEVDMEALSRMRYLKFESTMKRDPDTAQPLBELDEFQOTIDNWEPPVSCAFVVLMA 95
b 202 RGGVDVHSTLTFLKLLGYDVHVLCDTQAGMQEKLQNFQA-LPAHRTDSC-IVALLS 259
y 96 HGEGLLKGEDEKXVRLEDLFEVLANNKCKALRGPKVYIIQACRGHRDPGEELRGNEE 155
b 260 HGVEGAIYGVGKLLQLQEVFQFDNANCPSLQNKPKMFFIACRGDETDGVDQDQGN 319
y 156 LGQDEBLGGDEVAVLKNPQSIPTVTDTHIYSTVEGYLSYRHDCKSGFTQTLTDVFIH 215
b 320 HAGSPGCEBSDAGKEKLPKORLPTRSDMICGYACUKGTAAWNTYRGSGWYLEALQVF-S 378
y 216 KKGSIILELTFEITRLMANTENVMQGKPR-----KVNPEVQSTLRKKLYL 259
b 379 ERGCDMHVADMLVKVNAIKDREGVAPGTGFHRCCKEMSEYCGSTLCRHLYL 428

earch completed: March 19, 2004, 11:22:14
ob time : 55.8287 secs

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OM protein - protein search, using sw model

Run on: March 19, 2004, 11:17:55 ; Search time 34.7092 Seconds
(without alignments)

2199.863 Million cell updates/sec

Title: US-09-989-903-5

Perfect score: 1239

Sequence: 1 MSNPRSLERKDYMSGAALA.....KARKTNPEIQSTLRKELYIQ 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	24.1	452	11 Q8C9H7	Q8C9H7 mus musculus
2	295	23.8	452	11 Q8K241	Q8K241 mus musculus
3	293	23.6	452	11 Q55194	Q55194 rattus norv
4	289.5	23.4	423	13 Q91B67	Q91B67 xenopus lae
5	289	23.3	435	4 Q95UP7	Q95UP7 homo sapien
6	284.5	23.0	283	13 Q93417	Q93417 gallus gall
7	279.5	22.6	316	5 Q817B0	Q817B0 geodia cydo
8	279.5	22.6	426	5 Q816Y2	Q816Y2 geodia cydo
9	275.5	22.2	277	6 Q8MJC3	Q8MJC3 cryptolagus
10	275.5	22.2	277	6 Q8MTJ1	Q8MTJ1 felis silve
11	274.5	22.2	277	6 Q95ND5	Q95ND5 sus scrofa
12	274.5	22.2	383	13 Q919L7	Q919L7 brachydanio
13	273.5	22.1	313	11 Q8CHV5	Q8CHV5 mus musculus
14	272.5	22.0	277	6 Q8MK15	Q8MK15 canis fami
15	272	22.0	399	13 Q91B63	Q91B63 xenopus lae
16	270	21.8	303	11 Q88550	Q88550 rattus norv

Q9R0T0 mus musculu
Q90WU1 gallus gall
Q98UI8 brachydanio
Q8198 oryzias lat
Q83Q0 mus musculu
Q8C3Q9 mus musculu
Q86FL0 anopheles s
Q90WU0 gallus gall
Q918J3 brachydanio
Q91B64 xenopus lae
Q91B62 xenopus lae
Q9YIU6 pristionchu
Q9JHK1 rattus norv
Q8JGM9 figu rubrip
Q91B65 xenopus lae
Q8JG42 figu rubrip
Q81UP5 homo sapien
Q8BNT4 mus musculu
Q94089 mus musculu
Q8JIS9 oryzias lat
Q99M47 mus musculu
Q819V7 bombyx mori
Q81955 spodoptera
O77623 ovis aries
Q35397 rattus norv
Q81TP3 brachiosio
Q9JHX4 rattus norv
Q9GV89 hydra atten
Q9DDJ2 brachydanio

ALIGNMENTS

RESULT 1

Q8C9H7	PRELIMINARY;	PRT;	452 AA.
ID Q8C9H7			
AC Q8C9H7			
DT 01-VAR-2003 (TRENBLrel. 23, Created)			
DT 01-VAR-2003 (TRENBLrel. 23, Last sequence update)			
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)			
DE Caspase 2.			
GN CASP2.			
OS Mus musculus (Mouse)			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=C57BL/6J; TISSUE=Thymus;			
RX MEDLINE=22354683; PubMed=12466851;			
RA The FANTOM Consortium,			
RA the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT "Analysis of the mouse transcriptome based on functional annotation of			
RT 60,770 full-length cDNAs."			
RL Nature 420:563-573(2002).			
DR EMBL; AK042072; BAC31153.1; ..			
DR MGD; MGI:97295; Casp2.			
DR GO; GO:0005632; C:intracellular; IEA.			
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.			
DR GO; GO:0030693; F:caspase activity; IEA.			
DR GO; GO:0006915; P:apoptosis; IEA.			
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR InterPro; IPR001315; CARD.			
DR InterPro; IPR001309; ICE_P10.			
DR InterPro; IPR002138; ICE_P20.			
DR InterPro; IPR002398; Peptidase_C14.			
DR Pfam; PF00619; CARD; 1.			
DR Pfam; PF0856; Peptidase_C14; 1.			
DR PRINTS; PR00376; ILIBCNZYME.			
DR SMART; SM00114; CARD; 1.			
DR SMART; SM00115; CAS; 1.			
DR PROSITE; PS50209; CARD; 1.			

R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS50207; CASPASE_P10; 1.
R PROSITE; PS50208; CASPASE_P20; 1.
Q SEQUENCE 452 AA; 50689 MW; C3715908508619CA CRC64;
Query Match 24.1%; Score 298; DB 11; Length 452;
Best Local Similarity 31.9%; Pred. No. 5.8e-17;
Matches 76; Conservative 51; Mismatches 75; Indels 36; Gaps 7;
Y 29 REGSEEDLDALHMFRLQFESTMKDPTAEQFOBELEKFOQADSDREDPVSCAFVILMA 88
b 219 RSGGDVHTTLVTLFLKLGYNVHVLHDQTAQEMOEKLNQFAQ-LPAHRVTDSCV-VALLS 276
Y 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
b 277 HGVGGIYGVDGKLLQLOVEFLFDNANCPSLQNKPKMFFIQACRGETDGRGVDQDGKN 336
Y 141 -----ETVGGDEIVMWIKDSPQTIPTVTDALHVVSTVEGYIAYRHDKGSCFIQTLV 192
b 337 HTQSPGCEESDAGKEELMKMR-----LPTSDMICGYACILKGNAAMRNTKRGSWYIEALT 391
Y 193 DVFTKR--KGHILELLTEVTRMAEAELVOEGKARKTN-----PEIQSTLRKELYL 241
b 392 QVFSERACDMHADMVLKVNALIKE-----REGYAPGTFFHRCKEMSEYCSLCCQLYL 445
RESULT 2
ID Q8K241 PRELIMINARY; PRT; 452 AA.
AC Q8K241;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE CASP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034262; AA834262.1; -.
DR MGD; MGI197295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50661 MW; A4B25A712FAB855 CRC64;
Query Match 23.8%; Score 295; DB 11; Length 452;
Best Local Similarity 31.5%; Pred. No. 1e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Y 29 REGSEEDLDALHMFRLQFESTMKDPTAEQFOBELEKFOQADSDREDPVSCAFVILMA 88
b 219 RSGGDVHTTLVTLFLKLGYNVHVLHDQTAQEMOEKLNQFAQ-LPAHRVTDSCV-VALLS 276
Y 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
b 337 HTQSPGCEESDAGKEELMKMR-----LPTSDMICGYACILKGNAAMRNTKRGSWYIEALT 391
Y 193 DVFTKR--KGHILELLTEVTRMAEAELVOEGKARKTN-----PEIQSTLRKELYL 241
b 392 QVFSERACDMHADMVLKVNALIKE-----REGYAPGTFFHRCKEMSEYCSLCCQLYL 445

Db 219 RSGGDVHTTLVTLFLKLGYNVHVLHDQTAQEMOEKLNQFAQ-LPAHRVTDSCV-VALLS 276
Qy 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
Db 277 HGVGGIYGVDGKLLQLOVEFLFDNANCPSLQNKPKMFFIQACRGETDGRGVDQDGKN 336
Qy 141 -----ETVGGDEIVMWIKDSPQTIPTVTDALHVVSTVEGYIAYRHDKGSCFIQTLV 192
Db 337 HTQSPGCEESDAGKEELMKMR-----LPTSDMICGYACILKGNAAMRNTKRGSWYIEALT 391
Qy 193 DVFTKR--KGHILELLTEVTRMAEAELVOEGKARKTN-----PEIQSTLRKELYL 241
Db 392 QVFSERACDMHADMVLKVNALIKE-----REGYAPGTFFHRCKEMSEYCSLCCQLYL 445
RESULT 3
ID Q55194 PRELIMINARY; PRT; 452 AA.
AC Q55194;
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE NEDD2/ICH-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98087427; PubMed=9427555;
RA Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.;
RT "Cloning and expression of the cDNA encoding rat caspase-2";
RL Gene 202:127-132(1997).
DR EMBL; U77933; AA896379.1; -.
DR EMBL; AF136231; AA033684.1; -.
DR PIR; JC8507; JC6507.
DR HSSP; P29466; LICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50728 MW; 03F9D096B8741CE3 CRC64;
Query Match 23.6%; Score 293; DB 11; Length 452;
Best Local Similarity 31.5%; Pred. No. 1.5e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Qy 29 REGSEEDLDALHMFRLQFESTMKDPTAEQFOBELEKFOQADSDREDPVSCAFVILMA 88
b 219 RSGGDVHTTLVTLFLKLGYNVHVLHDQTAQEMOEKLNQFAQ-LPAHRVTDSCV-VALLS 276
Y 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
b 337 HTQSPGCEESDAGKEELMKMR-----LPTSDMICGYACILKGNAAMRNTKRGSWYIEALT 391
Y 193 DVFTKR--KGHILELLTEVTRMAEAELVOEGKARKTN-----PEIQSTLRKELYL 241
b 392 QVFSERACDMHADMVLKVNALIKE-----REGYAPGTFFHRCKEMSEYCSLCCQLYL 445

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277 HGVEGGYIGVDGKLLQLQEQVRLFDNANCPSLQNKPMFFIQACRGDETRGVDDQDGN 336
141 -----ETVGGDEIVMWIKDSPQIPYTDALHYSTVEGVIAVRHDKGSCFQTLV 192
337 HAQSPGCEESDAGKELMKVR-----LPTSDMICGYACLKGNAAWRNTKGSWTFEALT 391
193 DVFTKR--KGHILELLETVTRMAEAEALVQEGKARKTN-----PEIQSTLRKLYL 241
392 QVFSERACDMEVADMLVKVNALIKE----REGVAPGTETPHRCKEMSEYCTLCQQLYL 445

RESULT 4
991B67 PRELIMINARY; PRT; 423 AA.
ID Q91B67
AC Q91B67
DT 01-JUN-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Similar to caspase 2 (TrEMBLrel. 25, Last annotation update)
DE down-regulated 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RS SEQUENCE FROM N.A.
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002427; AAH02427.1; -.
DR EMBL; BC007240; AAP35904.1; -.
DR HSSP; P29466; IICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR Protease.
KW SEQUENCE.
SQ SEQUENCE 423 AA; 47123 MW; 531EB1FD133F01FD CRC64;

Query Match 23.4%; Score 289.5; DB 13; Length 423;
Best Local Similarity 30.5%; Pred. No. 2.8e-16;
Matches 74; Conservative 51; Mismatches 71; Indels 47; Gaps 7;

2Y 29 REGSEEDLDALEHMFQRLRFESTMKDPTAEQFQEELEK-----QAIDSREDPVSCAF 83
DB 187 RCGGEVDLASLEKLFSSLGUYQDVRCNLNQAQMSQSGAFSALPVHSALDS-----CV 239
2Y 84 VYLAHGEGLKGDGEMVKLENLFALNNKNCQALRAKPKVYIIQACRGEQDPG--- 140
DB 240 VAILSHGLDGAIVGTGDKLVQLQEVFTALDHAHCPQLONKPMFFIQACSGEETDRGVQ 299
2Y 141 -----ETVGGDEIVMWIKDSPQIPYTDALHYSTVEGVIAVRHDKGSCF 187
DB 300 RDGRQSGSPGCEQSDAGREDIKV-----RLPTQSDMI CAYACLKGTVSLRNTKGSWF 353
2Y 188 IOTLVVDVFTK--RKGHILELLETVTRMAEAEALVQEGKARKTN-----PEIQSTLRKR 238
```

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354 VDLVSVFQSHQKTHVADMLVKVNALIKE----REGHAPGTETPHRCKEMSEYCTLCRD 409
239 LYL 241
410 LYL 412

RESULT 5
Q99BUP7 PRELIMINARY; PRT; 435 AA.
ID Q99BUP7
AC Q99BUP7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to caspase 2 (Neural cell expressed, developmentally
DE down-regulated 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RS SEQUENCE FROM N.A.
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002427; AAH02427.1; -.
DR EMBL; BC007240; AAP35904.1; -.
DR HSSP; P29466; IICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR Protease.
KW SEQUENCE.
SQ SEQUENCE 435 AA; 48869 MW; 10CFASA1F9369E57 CRC64;

Query Match 23.3%; Score 289; DB 4; Length 435;
Best Local Similarity 31.1%; Pred. No. 3.2e-16;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

2Y 29 REGSEEDLDALEHMFQRLRFESTMKDPTAEQFQEELEKFOQAIDSREDPVSCAFVYVLA 88
DB 202 RSGGDVDSHTLVITFLKLLGYDVHVLCDTQAEQCKLQNFQAQ-LPAHRVTDSC-IVALLS 259
2Y 89 HGRGFLKGDGEMVKLENLFALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
DB 260 HGVEGGYIGVDGKLLQLQEQVRLFDNANCPSLQNKPMFFIQACRGDETRGVDDQDGN 319
2Y 141 -----ETVGGDEIVMWIKDSPQIPYTDALHYSTVEGVIAVRHDKGSCFQTLV 192
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b 320 HAGSPCESDSAGKE-----KLPKWLFRSRDMICGYACLGKTAAMRNTKSGSWYIALA 374
y 193 DVFTKR--KGHILELLTEVTRMAEAEVLQEGKARKTN-----PEIQSTLRKRLYL 241
b 375 QVFSERACDMHVDMLVKVNALIKD----REGYAPGTBFHRCKENSEYSCSTLCRHLYL 428

RESULT 6
93417 D 093417 PRELIMINARY; PRT; 283 AA.
C 083417;
T 01-NOV-1998 (TREMBlrel. 08, Created)
T 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
T 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
E Caspase-3.
S Gallus gallus (Chicken).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
C Gallus.
X NCBI_TaxID=9031;
N [1]
P SEQUENCE FROM N.A.
X MEDLINE=20149872; PubMed=10684799;
A Johnson A.L., Bridgman J.T.;
T "Caspase-3 and -6 expression and enzyme activity in hen granulosa
cells.";
L Biol. Reprod. 62:589-598(2000).
R EMBL; AF083029; AAC32602.1; -.
R HSP; P42574; IPAU.
R MEROPS; C14.003; -.
R GO; GO:0030693; F:caspase activity; IEA.
R InterPro; IPR002138; ICE_P10.
R InterPro; IPR001309; ICE_P20.
R Pfam; PF00656; Peptidase_C14.
R PRINTS; PR00376; ILIBENZYM.
R SMART; SM00115; CASG; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS0207; CASPASE_P10; 1.
R PROSITE; PS0208; CASPASE_P20; 1.
Q SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 23.0%; Score 284.5; DB 13; Length 283;
Best Local Similarity 30.3%; Pred. No. 4.6e-16;
Matches 76; Conservative 47; Mismatches 101; Indels 27; Gaps 7;

y 7 LEBEKYDMSGAALALILCVT-----KAREGSEEDLDALHMFRLQRPSTMKRDP 56
b 40 LPDDSYRMDYPEIGVCVVIINKNFHRDTGLSSKSGTDADAASVREVMKLGKVKLNNDL 99
y 57 TAQFQBELEKFOAIDSRDPVSCAFVVLMAHGREGLKGEDGMVKLENLFEALNNKN 116
b 100 SSRDIFKLLKNVSEEDHRSKSSVFC---VLLSGDDEGLFYGTGGL-ELKVLTSLFRGDK 155
y 117 COALRAKPKVYIIQACRGEQDPG--ETVGGBIWVINKDSPTIPTYTDALHVVSTVEG 174
b 156 CRSLAGKPKLFFIQAQCGTGLDSDGIEADSPDETVC-----QKIPVEADFLYAYSTAPG 209
y 175 YIAYRHQKSCFIQTLVDVFTK--RKGHILELLTEVTRMAEAEVL---QEGKARKTNP 229
b 210 YGWRNAEAGSWFIQSLCRLMKHARKLELMQLTRVNRRAVEYSCSTROQDFNAKKQIP 269
y 230 EIQSTLRKRLYL 240
b 270 CIVSMLTKEFY 280

RESULT 7
817B0 PRELIMINARY; PRT; 316 AA.
D Q817B0

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AC Q817B0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase 3.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417903; CAD10676.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
SQ SEQUENCE 316 AA; 35319 MW; 33A46BCCB6C3F9B7 CRC64;

Query Match 22.6%; Score 279.5; DB 5; Length 316;
Best Local Similarity 28.2%; Pred. No. 1.4e-15;
Matches 78; Conservative 54; Mismatches 94; Indels 51; Gaps 9;

Qy 9 EBYKMSG--AALAIL-----CVTKAREGSEEDLDALHMFRLQRPSTMKRDP 60
Db 37 KDAXMSSRPGRMALIINNRFTCGMKERVGTDKDAENLYGLFNWGLMATIRKDNLTGKA 96
Qy 61 FQBELEKFOAIDSRDPVSCAFVVLMAHGREGLKGEDGMVKLENLFEALNNKNQAL 120
Db 97 MTRFEDLARSDHSAVD---CVVAILTHGISGLYSTGDLIPVEDLTXYFDGVNRP 153
Qy 121 RAKPKVYIIQACRGEQDPG--ETVGG-----DEIVVVIKDSPT- 159
Db 154 ICKPKVYVQACRGGKFDYGVSESTDGEGSVNKNETANEMMERQFDKWEKALDADETD 213
Qy 159 -----IPTVTDALHVVSTVEGYIAYRHQKSCFIQTLVDVFE--TKRGHILELITE 208
Db 214 GGGYSREALPTADFLYAYAVPGVSVNRNSEYSGWFIKAFVDTWRDLASKEHFDILTE 273
Qy 209 VTRMAEAEVLQEGKARKTNPIQ---STLRKRLYLQ 242
Db 274 VNRKVA-----YDFQSRGRNKQIPAPVTMLTRKLYFR 305

RESULT 8
Q816Y2 PRELIMINARY; PRT; 426 AA.
AC Q816Y2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase-3.
GN CASP-3L.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Eukaryota;
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

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EMBL; AJ344144; CAC83013.1; -;
GO; GO:0030693; F:caspase activity; IEA.
InterPro; IPR00138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00656; Peptidase_C14; I.
PRINTS; PR00376; ILIBCNZYME.
SMART; SM00115; CASc; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
SEQUENCE 426 AA; 48024 MW; 713BSEC82RED0C1 CRC64;
Query Match 22.6%; Score 279.5; DB 5; Length 426;
Best Local Similarity 28.2%; Pred. No. 2e-15;
Matches 78; Conservative 54; Mismatches 94; Indels 51; Gaps 9;
2Y 9 EEKDMGSG--AALALIL-----CVTKAREGSEDLDALEHMFQRLRFSTMKRDPFAEQ 60
Db 147 KDAVMSSRPGRMALIINRNFTCGMKERVGTDKDAENLYGLFWNLGMATIRKDNLTGKA 206
2Y 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120
Db 207 MTRFEDLARRDHSAYD---CIVVAILTHGISGLYSTDGLIPVEDLTKYFDGVNRPDL 263
2Y 121 RAKPKVITIQACRGEQDPG---ETVGG-----DEIVMVKDSPT- 158
Db 264 IGKPKVFVQCACRGKDYGVSESTDGESYNKETANEMKQDFKVKVERALDADETD 323
2Y 159 -----IPYTDALHYSTVGTYAYRDQKSGCFIQLTVDF--TKRKHHLELLE 208
Db 324 GGGYSREALTEADFLVAYATVPYVSWRNSYGVSWFIFKAFVDVTRDLASKEHFMDILTE 383
2Y 209 VTRMAEAEVQEGKARKTNPEIQ---STLRKRLYLQ 242
Db 384 VNRKVA-----YDQSGRKNQIPAPVTMLTKLYR 415
RESULT 9
ID Q8MJU3 PRELIMINARY; PRT; 277 AA.
AC Q8MJU3
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Cysteine protease CPP32.
DC Oryctolagus cuniculus (Rabbit).
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
DX NCBI_TaxID=9986;
DX [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=98236830; PubMed=9575916;
RP Wang H., Keiser J.A.;
RP "Molecular characterization of rabbit CPP32 and its function in
RP vascular smooth muscle cell apoptosis.",
RP Am. J. Physiol. 274.H1132-H1140(1998).
RP [2]
RP SEQUENCE FROM N.A.
RP Wang H., Keiser J.A.;
RP Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RP EMBL; AF506008; AAM47195.1; -;
RP GO; GO:0030693; F:caspase activity; IEA.
RP GO; GO:0008233; F:peptidase activity; IEA.
RP GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
RP InterPro; IPR00138; ICE_P10.
RP InterPro; IPR001309; ICE_P20.
RP Pfam; PF00656; Peptidase_C14.
RP PRINTS; PR00376; ILIBCNZYME.
RP SMART; SM00115; CASc; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Protease.
SQ SEQUENCE 277 AA; 31653 MW; 7BA4B12E6D43629A CRC64;
Query Match 22.2%; Score 275.5; DB 6; Length 277;
Best Local Similarity 31.6%; Pred. No. 2.6e-15;
Matches 79; Conservative 39; Mismatches 105; Indels 27; Gaps 8;
QY 9 EEKDMGSGAALALILCVT-----KARGSEDLDALEHMFQRLRFSTMKRDPFA 58
Db 34 DNSYKMDYPENGLCIILNNKFNKNTGMSRSGTDVNAANLGETFWNLKYEVRNKNDLTR 93
QY 59 EQFQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQ 118
Db 94 EETWELMNVNVEDHKSRSFIC---VILSHDEGVIIYGTNGP-IELKLLISFFRGDYCR 149
QY 119 ALRAKPKVIIQACRGEQDPG-ETVGGDEIVVMVKDSFQTIPTVTDALHYSTVEGYIA 177
Db 150 SLATGKPLFIQACRGTSLDGIETDSGVYDMAC---QKIPVEADFLYAYSTAPGYIS 205
QY 178 YRHDQKSGCFIQLTVDFTKRKHHLE---LLTEYTRVA---EAEIVQEGKARKTNPE 230
Db 206 WRNSEGSGFIQSLC-AMUKYAHKLEFMHILTRNKRKVAITEFESYSLDAIFHAKKQIPC 264
QY 231 IQSTLRKRLY 240
Db 265 IVSMLTKELY 274
RESULT 10
ID Q8MJU1 PRELIMINARY; PRT; 277 AA.
AC Q8MJU1
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Caspase3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
OX [1]
RP SEQUENCE FROM N.A.
RP Yamazaki J., Sano J., Kano R., Hasegawa A.;
RP "Felis catus mRNA for caspase3, complete cds.",
RP Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RP EMBL; AB090246; BAC10589.1; -;
RP GO; GO:0030693; F:caspase activity; IEA.
RP GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
RP InterPro; IPR002138; ICE_P10.
RP InterPro; IPR001309; ICE_P20.
RP Pfam; PF00656; Peptidase_C14; 1.
RP PRINTS; PR00376; ILIBCNZYME.
RP SMART; SM00115; CASc; 1.
RP PROSITE; PS01122; CASPASE_CYS; 1.
RP PROSITE; PS01121; CASPASE_HIS; 1.
RP PROSITE; PS0207; CASPASE_P10; 1.
RP PROSITE; PS0208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31465 MW; 8749679C30AB46F6 CRC64;
Query Match 22.2%; Score 275.5; DB 6; Length 277;
Best Local Similarity 33.3%; Pred. No. 2.6e-15;
Matches 84; Conservative 35; Mismatches 102; Indels 31; Gaps 10;
QY 9 EEKDMGSGAALALILCVT-----KARGSEDLDALEHMFQRLRFSTMKRDPFA 58
Db 34 DNSYKMDYPENGLCIILNNKFNKNTGMSRSGTDVNAANLRETTNLKYEVRNKNDLTR 93
QY 59 EQFQEELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQ 118

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b 94 EQVALLDSVSRHDSKRSFTC---VLSHGEEGIIYGTNGP-VDLKKLTGFRGRCYCR 149
y 119 ALRAKPKVYIIQACRGEQDPG-ETVGG--DEIVMWIKDSPQTIPTTYDHALHYSTVEGY 175
b 150 SLTGKPLFIQACRGTELDGIGTDSGTEDDIAC-----QKIPVEADFLYAYSTAPGY 203
y 176 IAYHDQKSCFTQITVDVPTTKRGHILE---LLEVTTRMA-EAELVQEGKA---BKTN 228
b 204 YSRNKSQGSWFIQSCLSM-LRYAHELEFMEILTRVNRKVATEFESFLSDSAFHGKQI 262
y 229 PEIQSTLRKRLY 240
b 263 PCIVSMLTKELY 274

RESULT 11
9SND5 PRELIMINARY; PRT; 277 AA.
C Q95ND5;
T 01-DEC-2001 (T-EMBLrel. 19, Created)
T 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
T 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
E Caspase-3.
S Sus scrofa (Pig).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
X NCBI_TaxID=9823;
N [1]
P SEQUENCE FROM N.A.
X MEDLINE=21334413; PubMed=11440638;
A Muneta Y., Shimofujima Y., Mori Y.;
T "Porcine caspase-3: cloning and its activity during apoptosis of
L J. Interferon Cytokine Res. 21:409-415(2001).
L EMBL; AB029345; BAB55544.1; -.
R MEROPS; C14.003; -.
R GO; GO:0030693; P:caspase activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR002138; ICE_P10.
R InterPro; IPR001309; ICE_P20.
R InterPro; IPR002398; Peptidase_C14.
R Pfam; PF00656; Peptidase_C14; 1.
R PRINTS; PR00376; IL1BCENZME.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS50207; CASPASE_P10; 1.
R PROSITE; PS50208; CASPASE_P20; 1.
R SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 22.2%; Score 274.5; DB 6; Length 277;
Best Local Similarity 37.3%; Pred. No. 3.1e-15;
Matches 82; Conservative 27; Mismatches 94; Indels 17; Gaps 8;

y 29 REGSEEDLDALHMFRLQRFESTMKRDPDTAEQFQEBLEKFOQAIDSDREDVSCAFVILMA 88
b 64 RSGTDVDAANLRETFNLKYEVANKNDLTREETLELHMSVSKEDSKRSFTC---VLLS 120
y 89 HGREGLKSGDEGEVVKLENLFEALNNKNCALRAKPKVYIIQACRGEQDPG-ETVGGDE 147
b 121 HGEGLKIFGTNGP-VDLKKLTSTFRGDCRRLTGKPKLFIQACRGTELDGCIETDSGTE 179
y 148 IVMWIKDSPQTIPTTYDHALHYSTVEGYIAYRHDKGSCFIQTLVDVFTKRGHILEL-- 205
b 180 DDMAC---QKIPVEADFLYAYSTAPGYSWRNSKDGSWFIQSLCAAL-QYVVKLELMH 234
y 206 -LTVTRMA-EAELVQEGK---ARKTNPEIQSTLRKRLY 240
b 235 ILTRVNRKVAEFESFSTSTFFHAKQKQPCIVSMLTKELY 274

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RESULT 12

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Q919L7 PRELIMINARY; PRT; 383 AA.
AC Q919L7;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Caspase.
GN CASPA OR CASPY.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF233434; AAF66964.1; -.
DR HSSP; P29466; 1ICE.
DR ZFIN; ZDB-GENE-000616-3; caspa.
DR GO; GO:0030693; P:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR004020; PAAD_DAPIN_dom.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF02758; PAAD_DAPIN; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50824; DAPIN; 1.
DR SEQUENCE 383 AA; 43966 MW; 218908711309774C3 CRC64;

Query Match 22.2%; Score 274.5; DB 13; Length 383;
Best Local Similarity 30.0%; Pred. No. 4.7e-15;
Matches 69; Conservative 49; Mismatches 83; Indels 29; Gaps 6;

QY 29 REGSEEDLDALHMFRLQRFESTMKRDPDTAEQFQEBLEKFOQAIDSDREDVSCAFVILMA 88
Db 162 RSGSEKDEBNMEKLLKELDYQVVKENLSAKEMDEARDFAQREHKYS--DSAFVIVMS 219
QY 89 HGREGLKSG-----EDGEMVKLENLFEALNNKNCALRAKPKVYIIQACRGEQ--- 137
Db 220 HGKRDALMGVHYHRTNPNPSDSFPVDNVYRLNSENCPALRDKPKVILIQACRGEHGRVW 279
QY 138 ----DPGETVGDDEIVMWIKDSPQTIPTTYDHALHYSTVEGYIAYRHDKGSCFIQTLVD 193
Db 280 ASGGEFDEPIEDDDFVHKK-----DFISLMSCTPDKSYRHVQNGTFVQTLVD 331
QY 194 VFTK--RKGHILELLEVTTRMAEAELVQEGKARKTNPEIQSTLRKRLY 241
Db 332 VFTKCAHEDHIELEFRKVLRRPEHENMI--GNFKQMAKCKRATLPLKLYL 379

RESULT 13
Q8CHV5 PRELIMINARY; PRT; 313 AA.
AC Q8CHV5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Caspase 3, apoptosis related cysteine protease (Fragment).
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

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DR	PROSITE; PS01121; CASPASE_HIS; 1.
DR	PROSITE; P550207; CASPASE_P10; 1.
DR	PROSITE; P550208; CASPASE_P20; 1.
SQ	SEQUENCE 277 AA; 31334 MW; 7094C76D868BDAB9 CRC64;

Query Match	
Best Local Similarity	22.0%; Score 272.5; DB 6; Length 277;
Matches 84; Conservative	33.5%; Pred. No. 4.6e-15;
Mismatches 108; Indels 27; Gaps	

QY	9	EKYDMSGAALAILCVTK-----AREGSEDLDALEHMFQLRPFESTMKKDPTA 58
Dd	34	DSNYKMDYPENGLCGIINNNKNFHSTGWAPRSCTDYDAANLRFTFNLKYEVRLNKNDLTC 93
QY	59	EFOFELEKFFQAIDSRDPVSCAFVYLMAHGREGFLKGEDGMVKLENLFZALANNKCQ 118
Dd	94	ESILEMNSVKEHDKKRASSVC---VLLSGDEGIIFGTNGP-VDLRKVTGFPRGDYCR 149
QY	119	ALRAKPVIYIIACRGGEORDFG-ETVGSDBIWVMIKDSPQTIFTYTDLHVYSTVEGYIA 177
Dd	150	SLTGPKPLFIICAKRGTELDGCIETDSGIEDDMAC----QKIPEADFLVAYSTAPGYYS 205
QY	178	YHDOKGSCFTVLVDVFTRKKGHILS---LLETVTRMA-EAELVQEGKA--RKTNPE 230
Dd	206	WNNSXDGSGWFQISLC-AMLKUYAHKLEFMHILTRVNKRVATEFESLSDSAFHGKKQIEC 264
QY	231	IQSTLRKELYL 241
Dd	265	IIVSMLTKEYL 275

RESULT 15		
Q9IB63		
ID	C9IB63	PRELIMINARY; PRT; 399 AA.
AC	Q9IB63;	
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	Caspase-9.	
GN	KCASPASS-9.	
OS	Xenopus laevis (African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
OC	Xenopodinae; Xenopus.	
NCBI_Taxid=8355;		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20209426; PubMed=10744739;	
RA	Nakajima K., Takahashi A., Yacita Y.;	
RT	"Structure, expression and function of the Xenopus laevis caspase family.";	
RL	J. Biol. Chem. 275:10484-10491 (2000).	
RE	EMBL; AB038172; BAA94750.1; -.	
DR	HSSP; Q15806; IQDU.	
DR	MEROPS; C14.010; -.	
DR	GO; GO:0005622; C:intracellular; IEA.	
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.	
DR	GO; GO:0030693; F:caspase activity; IEA.	
DR	GO; GO:0006915; F:apoptosis; IEA.	
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.	
DR	GO; GO:0007165; P:signal transduction; IEA.	
DR	InterPro; IPR001315; CARD.	
DR	InterPro; IPR000488; Death.	
DR	InterPro; IPR002138; ICE p10.	
DR	InterPro; IPR001309; ICE p20.	
DR	InterPro; IPR002398; Peptidase_C14.	
DR	Pfam; PF00619; CARD; 1.	
DR	Pfam; PF00656; Peptidase C14; 1.	
DR	PRINTS; PRO0376; ILIBCENZME.	
DR	SMART; SM00114; CARD; 1.	
DR	SMART; SM00115; CASC; 1.	
DR	PROSITE; P550209; CARD; 1.	
DR	PROSITE; P501122; CASPASE_CYS; 1.	
DR	PROSITE; PS01121; CASPASE_HIS; 1.	

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R PROSITE; PS50207; CASPASE P10; 1.
R PROSITE; PS50208; CASPASE P20; 1.
R PROSITE; PS50017; DEATH DOMAIN; 1.
Q SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match      22.0%; Score 272; DB 13; Length 399;
Best Local Similarity 27.9%; Pred. NO. 8e-15;
Matches 80; Conservative 40; Mismatches 107; Indels 60; Gaps 8;

Y 2 SNFRSLEEEK-YDMSGAAALALILCVT-----KAREGSEEDLDALAHMFRLRFES 50
b 125 SRKGTLDKDKDYPMSSDPDIFGCLIIINNMNFHECTGLSTRGSDIDRDKLANRMSFHFV 184
Y 51 TMKRDPTAQFQEELEKFOQAIDSRDPVSCAFVVLMAHGRE-----GFLKGEDGEMV 103
b 185 TVKONLTGQAMHDLQALADQDHSLOD---CCLWLILSHGCETRIQFFGGVYGTGIRI 241
Y 104 KLENLPEALNNKNCQALRAKPKYIIQACGEGQDPGETVGG----- 145
b 242 FVERIVSYFNGSKCPSLRGKPKFIILQACGQDKQKGCVEVSETPLSPTSTLSQSDATP 301
Y 146 -----DEIVNVIKDSPQTIPTTDTALHVIYSTVEGYIAYRHQKSGCFIQTLLVDVFTK 197
b 302 VFSGEGDRDEV-----DAVSNIEPTSDILVSYSTFPGYVSWRDKHTGSMYVEVLDSVLAE 356
Y 198 RKG--HILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKGLYLQ 242
b 357 HAAADQLQSLVMV-----ADGVSSKGYKQIPGYFNFRLKRFYFK 397
```

earch completed: March 19, 2004, 11:24:12
ob time : 35.7092 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: March 19, 2004, 11:09:05 ; Search time 9.64143 seconds
(without alignments)
1306.961 Million cell updates/sec

title: US-09-989-903-5

effect score: 1239

sequence: 1 MSNPRSLBEKYMGAALA.....KARKTNPEIQTLRLRLYLQ 242

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 141691 seqs, 52070155 residues

total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	1	ICEE_HUMAN
2	934.5	75.4	257	1	ICEE_MOUSE
3	305	24.6	424	1	ICEE_CHICK
4	295	23.8	435	1	ICEE_MOUSE
5	289	23.3	435	1	ICEE_HUMAN
6	279.5	22.6	277	1	ICEE_RAT
7	277.5	22.4	277	1	ICEE_CRLO
8	273.5	22.1	277	1	ICEE_MOUSE
9	272.5	22.0	277	1	ICEE_HUMAN
10	270	21.8	303	1	ICEE_MOUSE
11	260	21.0	303	1	ICEE_MOUSE
12	256	20.7	303	1	ICEE_MOUSE
13	248.5	20.1	503	1	ICED3_CAEEL
14	247.5	20.0	339	1	ICED3_ERONE
15	246.5	19.9	479	1	ICED3_HUMAN
16	245	19.8	496	1	ICED3_CAEVU
17	240.5	19.4	276	1	ICED3_MOUSE
18	239.5	19.3	416	1	ICED3_HUMAN
19	237.5	19.2	299	1	ICEL1_SPOFR
20	236.5	19.1	404	1	ICED3_CANFA
21	233	18.8	480	1	ICED3_MOUSE
22	227	18.3	382	1	ICED3_XENLA
23	226.5	18.3	382	1	ICED3_XENLA
24	226	18.2	404	1	ICED3_HUMAN
25	225.5	18.2	323	1	ICED3_DROME
26	225	18.2	418	1	ICED3_HUMAN
27	222.5	18.0	385	1	ICED3_XENLA
28	222	17.9	293	1	ICED3_HUMAN
29	221.5	17.9	521	1	ICED3_HUMAN
30	218.5	17.6	402	1	ICED3_RAT
31	218	17.6	373	1	ICED3_MOUSE
32	217.5	17.6	402	1	ICED3_MOUSE
33	213.5	17.2	312	1	ICED3_RAT

RESULT 1				
ICED3_HUMAN				
ID	ICED3_HUMAN	STANDARD;	PRT;	242 AA.
AC	P31944; O95823;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Caspase-14 precursor (EC 3.4.22.-) (CASP-14).			
GN	CASP14.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	TISSUE=Brain;			
RX	MEDLINE=22168928; PubMed=12181750;			
RA	Pistritto G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,			
RA	Kari C., Lazebnik Y., Rodeck U., Alnemri E.S.;			
RT	"Expression and transcriptional regulation of caspase-14 in simple			
RT	and complex epithelia."			
RL	Cell Death Differ. 9:995-1006(2002).			
RN	[2]			
RP	SEQUENCE OF 68-74; 137-147 AND 154-162.			
RC	TISSUE=keratinocytes;			
RX	MEDLINE=93162043; PubMed=1286667;			
RA	Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,			
RA	Van der Kerckhove J.;			
RT	"Microsequences of 145 proteins recorded in the two-dimensional gel			
RT	protein database of normal human epidermal keratinocytes.";			
RL	Electrophoresis 13:960-969(1992).			
CC	-!- FUNCTION: May be involved in the death receptor and granzyme B			
CC	apoptotic pathways. May function as a downstream signal transducer			
CC	of cell death.			
CC	-!- SUBUNIT: May dimerize with large prodomain caspases.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-!- SIMILARITY: Belongs to peptidase family C14.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF097874; AAD16173.1; ..			
DR	PIR; JC7517; JC7517.			
DR	HSSP; P29466; ICCE.			
DR	Aarhus/Ghent-2DPAGE; 6109; IEF.			
DR	MEROPS; C14.018; ..			
DR	Genew; HGNC:1502; CASP14.			
DR	MIN; 605848; ..			
DR	GO; GO:0004199; F:caspase activity; TAS.			
DR	GO; GO:0008544; P:epidermal differentiation; TAS.			
DR	InterPro; IPR002138; ICE_p10.			

Q9tv13 equus caballus
Q9mv6 felis silvestris
Q9n211 sus scrofa
P49662 homo sapiens
O75601 bos taurus
O08736 mus musculus
O08736 mus musculus
O35732 m. casp8 and
O60039 emricella
Q87wh1 pseudomonas
Q9be52 macaca fasciata
O14157 schizosaccharomyces
O15519 h. casp8 and

ALIGNMENTS


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3 InterPro; IPR001309; ICE_P20.
4 InterPro; IPR002398; Peptidase C14.
5 Pfam; PF00656; Peptidase C14; 1.
6 PRINTS; PR00376; ILBCEZYME.
7 SMART; SM00115; CASc; 1.
8 PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
9 PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
10 PROSITE; PS0207; CASPASE_P10; 1.
11 PROSITE; PS0208; CASPASE_P20; 1.
12 Hydrolase; Thiol protease; Apoptosis; Zymogen.
13 PROPEP 1 ?
14 CHAIN ? 146
15 SUBUNIT ? 146
16 TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain and kidney.
17 ACT_SITE 89 89
18 ACT_SITE 132 132
19 SEQUENCE 242 AA; 27679 MW; E539F7E8DD808A2 CRC64;

Query Match 99.6%; Score 1234; DB 1; Length 242;
Best Local Similarity 99.6%; Pred. No. 5.8e-92;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 1 MNSPRLEEKYDMSGALALILCVTKAREGSEDDLDALHMFQRLFEFTMKRDPDAEQ 60
2 1 MNSPRLEEKYDMSGARLALILCVTKAREGSEDDLDALHMFQRLFEFTMKRDPDAEQ 60
3 61 FOELEKFOAIDSDREDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQCAL 120
4 61 FOELEKFOAIDSDREDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQCAL 120
5 121 RAKPKVYIIQACRGQRDPGEVGVGDEIVWIKSPQIPIYTDALHYSTVEGYIAYRH 180
6 121 RAKPKVYIIQACRGQRDPGEVGVGDEIVWIKSPQIPIYTDALHYSTVEGYIAYRH 180
7 181 DQKSGCFIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKNPFIQSTLRKELY 240
8 181 DQKSGCFIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKNPFIQSTLRKELY 240
9 241 LQ 242
10 241 LQ 242

ESULT 2
CEE MOUSE STANDARD; PRT; 257 AA.
C Q89034;
T 16-OCT-2001 (Rel. 40, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 15-MAR-2004 (Rel. 43, Last annotation update)
E Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mini-ICE) (MICE).
N CASP14.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
P STRAIN=C57BL/6J;
X MEDLINE=99040667; PubMed=9823333;
A Ahmad M., Srinivasula S.M., Hegde R., Mukattash R.,
A Fernandes-Alnemri T., Alnemri E.S.,
A "Identification and characterization of murine caspase-14, a new
T member of the caspase family.";
L Cancer Res. 58:5201-5205(1998).
[2]
SEQUENCE FROM N.A.
P STRAIN=C57BL/6; TISSUE=Embryo;
X MEDLINE=99222069; PubMed=10203698;
A Van de Craen M., Van Ico G., Pyne S., Van Crieckinge W.,
A Vandenabeele P.,
A "Identification of a new caspase homologue: caspase-14.";
T Cell Death Differ. 5:838-846(1998).
L

```

(3)

CHARACTERIZATION, AND MUTAGENESIS OF CVS-136.

MEDLINE=99009076; PubMed=9792675;

Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.;

"Caspase-14 is a novel developmentally regulated protease.";

J. Biol. Chem. 273:29648-29653(1998).

B FUNCTION: Seems to be involved in the death receptor and granzyme B apoptotic pathways. May function as a downstream signal transducer of cell death. May play a role in ontogenesis and skin physiology.

CC SUBUNIT: May dimerize with large prodomain caspases.

CC SUBCELLULAR LOCATION: Cytoplasmic (By similarity)

CC TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain and kidney.

CC PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE

CC SIMILARITY: Belongs to peptidase family C14.

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EMBL; AF092997; AAC63364.1; -

EMBL; AJ007750; CAA07678.1; -

HSSP; P29466; 1ICE.

MEROPS; C14.018; -

MGD; MGI:1335092; Casp14.

GC; GO:0006917; P:induction of apoptosis; IDA.

InterPro; IPR002138; ICE_P10.

InterPro; IPR001309; ICE_P20.

InterPro; IPR002398; Peptidase_C14.

Pfam; PF00656; Peptidase_C14; 1.

PRINTS; PR00376; ILBCEZYME.

SMART; SM00115; CASc; 1.

PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.

PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.

PROSITE; PS0207; CASPASE_P10; 1.

PROSITE; PS0208; CASPASE_P20; 1.

KW Hydrolase; Thiol protease; Apoptosis; Zymogen.

FT PROPEP 1 7

FT CHAIN 8 8 ?

FT CHAIN 2 257

FT ACT_SITE 93 93

FT ACT_SITE 136 136

FT MUTAGEN 136 136

FT C->A: DECREASE IN DEATH-INDUCING ACTIVITY.

SQ SEQUENCE 257 AA; 29458 MW; A228D89DFBA0EB84 CRC64;

Query Match 75.4%; Score 934.5; DB 1; Length 257;

Best Local Similarity 70.9%; Pred. No. 6.5e-68;

Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MNSPRLEEKYDMSGALALILCVTKAREGSEDDLDALHMFQRLFEFTMKRDPDAEQ 60

DB 5 MSDPQLOEERYDMSGARLALILCVTKAREGSEDDLDALHMFQRLFEFTMKRDPDAEQ 64

QY 61 FOELEKFOAIDSDREDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQCAL 120

DB 65 FLEELDEFQQTIDNWESEPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQCAL 124

QY 121 RAKPKVYIIQACRGQRDPGEVGVGDEIVWIKSPQIPIYTDALHYSTVEGYIAYRH 168

DB 125 RAKPKVYIIQACRGQRDPGEVGVGDEIVWIKSPQIPIYTDALHYSTVEGYIAYRH 183

QY 169 YSTVEGYIAYRHDKGSCFIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKNP 228

DB 184 YSTVEGYIAYRHDKGSCFIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKNP 243

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229 PEOSTLRKLYLQ 242
244 PEVOSTLRKLYLQ 257

RESULT 3
ICE2 CHICK STANDARD; PRT; 424 AA.
ID Q98943;
YI 01-NOV-1997 (Rel. 35, Created)
YI 01-NOV-1997 (Rel. 35, Last sequence update)
YI 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).
DE CASP2 OR ICH1.
DE Gallus gallus (Chicken).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
DE Gallus.
DE NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
RC STRAIN=White leghorn; TISSUE=Ovarian granulosa;
RX MEDLINE=97368127; PubMed=9224894;
RA Johnson A.B., Bridgman J.T., Bergeron L., Yuan J.;
RT "Characterization of the avian Ich-1 cDNA and expression of Ich-1L
RT mRNA in the hen ovary.";
RL Gene 192:227-233(1997).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=ICH-1L;
CC IsoId=Q98943-1; Sequence=Displayed;
CC Note=Only form found in the ovary;
CC Name=ICH-1S;
CC IsoId=Q98943-2; Sequence=VSP 000804;
CC -!- PTM: Heterodimer of a small and a large subunit (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
DR EMBL: U64963; AAC29881.1; ALT_INIT.
DR HSP: P42574; ICP3.
DR MEROPS: C14.006; .
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILIACENZYME.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CARD; 1.
DR PROSITE: PS0209; CARD; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
KW Hydroxylase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
FT PROPEP 1 140
FT CHAIN 141 308 BY SIMILARITY.
FT CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
FT FEBS Lett. 403:61-69(1997).
FT CHAIN 309 424
FT CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
FT FEBS Lett. 403:61-69(1997).

FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
FT DOMAIN 7 96 CARD.
FT ACT_SITE 248 248 BY SIMILARITY.
FT ACT_SITE 291 291 Missing (in isoform ICH-1S).
FT VARSPLIC 1 7 /FTId=VSP 000803.
FT VARSPLIC 294 424 DETDREVDDQKRSDDSPGCEESDANKENIKLELPTRSD
MICGACLGTAAMNTRKGSWYIALITVFAEDSRDTHVA
DMLVKNRQIKRGEGYAPGTEFHRCKEMSEYCSLCLRDLYL
FPQYVFGK -> GVSQIHLPLPCCHCICCSMRQTGEWI
REMAKNGQIPQAVRRVMQTRKKISSCVCLHAPI (in
isoform ICH-1S).
/FTId=VSP 000804.
SQ SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;

Query Match 24.6%; Score 305; DB 1; Length 424;
Best Local Similarity 31.5%; Pred. No. 3.7e-17;
Matches 86; Conservative 51; Mismatches 82; Indels 54; Gaps 10;

QY 1 MSNPRSEEEKYDMSGAALALILC-----VTKAREGSEEDLDALHMPRQLAFESTM 52
DB 166 ISBPR-----GLALLILSNTHFSKXDLVRSQGVDDCASLELLFKHLGYQTV 213
QY 53 KRDPFAEQFELEKFOQAIIDSRDPVSCAFVYVMAHGREGLKGDGEMVXLENLFPAL 112
DB 214 FHDQSAEMESALERSFKLPD-HQVDVSC-IVALLSHGVGGVGTGDKLLOLQEAFLF 271
QY 113 NKKVCOALRAKPYVLIQACRGQRDPG-ETVGGDEIVNVIKDSP-----Q 157
DB 272 DNANCPNLQNKPKMFFIQACRGDETRGVDQDQDGE-----RSDSPGCEESDANKENIKL 327
QY 158 TIPTYTDALHVVSTVEGYIAYRHQDGSCFIOQLVDVFTK--RKHILELLTEVTRRAE 215
DB 328 RLPRSDMICGYACLGTAAMNTRKGSWYIALITVFAEDSRDTHVADMLVKNRQIKQ 387
QY 216 AELVQEGKARKTN-----PEQSTLRKLYL 241
DB 388 ----REGYAPGTEFHRCKEMSEYCSLCLRDLYL 416

RESULT 4
ICE2 MOUSE STANDARD; PRT; 435 AA.
ID IC82_MOUSE STANDARD; PRT; 435 AA.
AC P29594; O08737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2
DE protein).
GN CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
RT protein similar to the product of the Caenorhabditis elegans cell
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RN [3]
FEBS Lett. 403:61-69(1997).
```

P PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 TISSUE=Brain;
 MEDLINE=92228780; PubMed=1378265;
 Kumar S., Tomooka Y., Noda M.;
 "Identification of a set of genes with developmentally down-regulated
 expression in the mouse brain."
 Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
 -!- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Might function by either
 activating some proteins required for cell death or inactivating
 proteins necessary for cell survival. May be important in
 multistep carcinogenesis.
 -!- SUBUNIT: Heterodimer of a small and a large subunit (By
 similarity).
 -!- TISSUE SPECIFICITY: High level expression seen in the embryonic
 CNS, liver, lung, kidney, small intestine, and hair follicles of
 vibrissae. Moderate expression seen in the skin, oral mucosa,
 skeletal muscle, submandibular gland and thymus. In the adult, it
 is highly expressed in spleen, lung and kidney. Moderately in the
 brain, heart, testis, liver. Low levels in the thymus, skeletal
 muscle, ovary and gut.
 -!- DEVELOPMENTAL STAGE: During embryonic development is highly
 expressed in several types of mouse tissue undergoing high rates
 of programmed cell death such as central nervous system and
 kidney.
 -!- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
 THAT OF OTHER CASPASES (BY SIMILARITY).
 -!- SIMILARITY: Belongs to peptidase family C14.
 -!- SIMILARITY: Contains 1 CARD domain.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).

 EMBL: D28492; BAA25876.1; ALT INIT.
 EMBL: Y12085; CAA73527.1; ALT_INIT.
 HSP: P42574; ICP3.
 MEROPS: C14.006; -.
 MGD: MGI:97295; Casp2.
 InterPro: IPR001315; CARD.
 InterPro: IPR002138; ICE_P10.
 InterPro: IPR001309; ICE_P20.
 InterPro: IPR002398; Peptidase_C14.
 Pfam: PF00619; CARD; 1.
 Pfam: PF00656; Peptidase_C14; 1.
 PRINTS: PR00376; ILIBENZYME.
 SMART: SM00114; CARD; 1.
 SMART: SM00115; CASC; 1.
 PROSITE: PS50209; CARD; 1.
 PROSITE: PS01122; CASPASE_CYS; 1.
 PROSITE: PS01121; CASPASE_HIS; 1.
 PROSITE: PS02077; CASPASE_P10; 1.
 PROSITE: PS02078; CASPASE_P20; 1.
 Hydrolase; Thiol protease; Apoptosis; Zymogen.
 PROPEP 1 152
 BY SIMILARITY.
 T CHAIN 153 316
 CASPASE-2 SUBUNIT P10 (BY SIMILARITY).
 T CHAIN 317 435
 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
 T CHAIN 331 435
 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
 T DOMAIN 15 103
 CARD.
 T ACT_SITE 260 260
 BY SIMILARITY.
 T ACT_SITE 303 303
 BY SIMILARITY.
 T MUTAGEN 303 303
 C->G: LOSS OF FUNCTION.
 T CONFLICT 71 71
 MISSING (IN REF. 1).
 Q SEQUENCE 435 AA; 48896 MW; 8984E6AA767A676 CRC64;

Query Match 23.8%; Score 295; DB 1; Length 435;
 Best Local Similarity 31.5%; Pred. No. 2.4e-16;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 REGSEEDLDALEHMFRLQRFESTWKRDPETAQOFELEKFKQQAIDSRDPVSCAFVILMA 88
 Db 202 RSGGDVHTTLVTLFKLLGYNVHVLHDQTAQEMQKQLQFAQ-LPAHRVTDSCV-VALLS 259
 QY 89 HGRGFLKGDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQBDPG----- 140
 Db 260 HGVEGGYGVGDKLLQJQEVFRFLFDNANCSLQNKPKMFFIQACRDETDGVDQDQGN 319
 QY 141 -----ETVGGDEIVWVKDSPTIPTYTDALHYVSTVEGYIAYRHQKSCFIQTIV 192
 Db 320 HTQSPGCESDAGKEELMKVR-----LPTSDMICGVACLKGNAAEMTKRGSWYTEALT 374
 QY 193 DVFTKR--KGHILELLETVTRMAEALVQSGKARKTN-----PEIQSTLEKRLYL 241
 Db 375 QVFSERACDMHVDMLVKVNAIKE----REGYAGTFEHRCKEMSEYCSLCCQQLYL 428
 RESULT 5
 ICE2 HUMAN
 ID ICE2 HUMAN STANDARD; PRT: 435 AA.
 AC P42575; P42576;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
 1L/1S)
 GN CASP2 OR ICH1
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Fetal brain;
 RX MEDLINE=94373811; PubMed=8087842;
 RA Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
 "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
 regulators of programmed cell death."
 RT Cell 78:739-750(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND
 RP GLY-424.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson F.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Doeber A., Martinka S., Maupin R.;
 Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP CLEAVAGE SITES.
 RX MEDLINE=96206041; PubMed=8654923;
 RA Xue D., Shaham S., Horvitz H.R.;
 "The Casorhabditis elegans cell-death protein CED-3 is a cysteine
 protease with substrate specificities similar to those of the human
 CPP32 protease."
 RT Genes Dev. 10:1073-1083(1996).
 RL CC
 -!- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Might function by either
 activating some proteins required for cell death or inactivating
 proteins necessary for cell survival.
 -!- SUBUNIT: Heterodimer of a small and a large subunit (By
 similarity).
 -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Isoforms differ in the N- and C-termini;
 CC Name=ICH-1L;
 CC IsoID=P42575-1; Sequence=Displayed;
 CC Note=Acts as a positive regulator of apoptosis;
 CC Name=ICH-1S;
 CC IsoID=P42575-2; Sequence=VSP 000801, VSP_000802;
 CC Note=Acts as a negative regulator of apoptosis;

-!- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic lung, liver and kidney than in the heart and brain. In the adults higher level expression is seen in the placenta, lung, kidney, pancreas than in the heart, brain, liver and skeletal muscle.
 -!- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT THAT OF OTHER CASPASES.
 -!- SIMILARITY: Belongs to peptidase family C14.
 -!- SIMILARITY: Contains 1 CARD domain.

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 EMBL; U13021; AAA58959.1; --
 EMBL; U13022; AAA58960.1; --
 EMBL; AY219042; ARO25653.1; --
 EMBL; AC073342; AAP22346.1; --
 PIR; A54821; A54821.
 HSP; P29466; 1ICE.
 MEROPS; C14.006; --
 Genew; HGNC:1503; CASP2.
 MIM; 600639; --
 GO; GO:0004202; F:caspase-2 activity; TAS.
 GO; GO:0019899; F:enzyme binding; TAS.
 GO; GO:000632; P:apoptotic program; TAS.
 GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 InterPro; IPR001315; CARD.
 InterPro; IPR002138; ICE_p10.
 InterPro; IPR001309; ICE_p20.
 InterPro; IPR002398; Peptidase_C14.
 Pfam; PF00656; CARD; 1.
 PRINTS; PR00376; IL1BCENZYM.
 SMART; SMO0114; CARD; 1.
 SMART; SMO0115; CASG; 1.
 PROSITE; PS02029; CARD; 1.
 PROSITE; PS01122; CASPASE_CYS; 1.
 PROSITE; PS01121; CASPASE_HIS; 1.
 PROSITE; PS02027; CASPASE_P10; 1.
 PROSITE; PS02028; CASPASE_P20; 1.
 Hydrolase; Thiol protease; Apoptosis; Zymogen; Polymorphism;
 Alternative splicing
 PROPEP 1 152 CASPASE-2 SUBUNIT P18.
 CHAIN 153 308 PROPEP
 PROPEP 309 316 CASPASE-2 SUBUNIT P13.
 CHAIN 317 435 CASPASE-2 SUBUNIT P12.
 CHAIN 331 435 CARD.
 DOMAIN 15 103 BY SIMILARITY.
 ACT_SITE 260 260 BY SIMILARITY.
 ACT_SITE 303 303 Missing (in isoform ICH-18).
 VARSPLIC 1 14 /FTid=VSP_000801.
 VARSPLIC 306 435 DETDRGVQDDGKNGHAGSPGCEESDAGKELPKMRLPTRSD
 MICGYACLGKTAAMRNKRGSWYIEALAOVFSERACDMHVA
 DMLVKVNALIKREGVAPGPEPHCKEMSEYCSLCHLYL
 PPGHEPT -> GGNIGSLGHLILFTATASLAL (in isoform ICH-18).
 /FTid=VSP_000802.
 V -> L. /FTid=VAR_016334.
 P -> A. /FTid=VAR_016335.
 R -> G. /FTid=VAR_016336.
 C -> S. LOSS OF FUNCTION.
 A -> T. LOSS OF FUNCTION.
 SEQUENCE 435 AA; 48855 MW; 1652EC73F6286E97 CRC64;
 Query Match 23.3%; Score 289; DB 1; Length 435;

Best Local Similarity 31.1%; Pred. No. 7.3e-16;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
 QY 29 REGSEDLDALEHMFRLQRFESTMKRDPDTAEQFOBELEKFOQADSDREDPVSCAFVVLMA 88
 DB 202 RSGGDVHSTLTVLFLKLLGYDVHVLCDQTAQEMQKLFQAFQ-UPAHRVTDSC-IVALLS 259
 QY 89 HGREGLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDFG----- 140
 DB 260 HGVEGAIYGVQDKLLQLQVLFQDFNANCPSLQNKPKMFFIQAQCKGDETDGRVQDDQGN 319
 QY 141 -----FTVGDEIVMWIKSPOTITTYTDALHVSTVEGYIAYRHDQKSGFIQTLV 192
 DB 320 HAGSPCEESDAGKE-----KLPKMRLPTRSDMICGYACLGKTAAMRNKRGSWYIEALA 374
 QY 193 DVFTKQ--KGHILELITVTRMAEALVQEGKARKTN-----PEIQSLRKRLYL 241
 DB 375 QVFSERACDMHVMVKNALIKD-----REGVAGTEFHRCKEMSEYCSLCHRLYL 428

 RESULT 6
 ID ICE3 RAT STANDARD; PRT; 277 AA.
 AC P55213; P70543; P97699; Q62993;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (BC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1) (SCA-1) (LICE) (IRP).
 DE (SCA-1) (LICE) (IRP).
 GN CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher F.A.,
 RA "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme RT and CED-3".
 RL Oncogene 13:749-755(1996).
 [2]
 RP SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I., Hirshfield A.N., Tilly J.L.;
 RA "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cells of the ovarian follicle".
 RL Endocrinology 136:5042-5053 (1995).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184204; PubMed=9030616;
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K., Rostek P. Jr., Poirier G.G., Paul S.M.;
 RA "Cloning and expression of a rat brain interleukin-1beta-converting enzyme (ICE)-related protease (IRP) and its possible role in apoptosis of cultured cerebellar granule neurons".
 RL J. Neurosci. 17:1561-1569(1997).
 [4]
 RP SEQUENCE OF 1-264 FROM N.A.
 RA Yakovlev A.G.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. At the onset of apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp|-Gly-217 bond. Cleaves and activates sterol regulatory

[illegible]

Query Match	22.6%;	Score 279.5;	DB 1;	Length 277;
Best Local Similarity	32.8%;	Pred. No. 2.4e-15;		
Matches	82;	Conservative 35;	Mismatches 106;	Indels 27; Gaps 8;
y	9	EKKYDSGAALALILCVT-----KARGSEEDLDALEHFRQLRPFSTMKRPTA	58	
b	34	DSQKYDYPENGLCIIINNNKNTHKSTGSAANGTVDAAANLEEFMAKVYRNKDLTR	93	
y	59	EQFQEELERQQQAIDSRDPVSCAFVYLMAHGREGFLXGDEGMVKLENLFALNNKCQ	118	

PRINTS; PRO0376; IL1BENZYMES.
RA SMART; SM0115; CASc; 1.
RA PROSITE; PS01122; CASPASE_CYS; 1.
RA PROSITE; PS01121; CASPASE_HIS; 1.
RA PROSITE; PS0207; CASPASE_P10; 1.
RA PROSITE; PS0208; CASPASE_P20; 1.
W Hydrolyase; Thiol protease; Zymogen; Apoptosis.
T PROPEP 1 9 BY SIMILARITY.
T PROPEP 10 28 APOAIN P17 SUBUNIT.
T CHAIN 29 175 APOAIN P12 SUBUNIT.
T CHAIN 176 277 APOAIN P12 SUBUNIT.
T ACT_SITE 121 121 BY SIMILARITY.
T ACT_SITE 163 163 BY SIMILARITY.
Q SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;
Query Match 22.4%; Score 277.5; DB 1; Length 277;
Best Local Similarity 35.9%; Pred. No. 3.4e-15;
Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;
Y 29 REGSEDLDALEHMFRLRFSTWMDPTAQFQBELEKFAIDSRDFVSCAFVVLMA 88
b 64 RSGTVDAAKLRETFWALKYEVKNKDLTREIEVLMKNASKEDSKRSFVC---VILS 120
Y 89 HGRGFLKGGEGWKLNFLEALNNKNCALRAKPVIIQACGEORDPG-ETVCGDE 147
b 121 HGDDEVFTGDP-IDLKLTSVFRGDYKSLICKPLFIQACRGTELDGCIETDSGTE 179
Y 148 IVWIKDSPTPTPTDHALHYSTVEGYTAHRDQKSGCFITGLVDVFFPKRGHILE--- 204
b 180 DDMTC---QKIPVADFLVAYSTAPGYYSWRNPKDGSWFIQSLCSML-KLYAHKLEFVH 234
Y 205 LITVTRMA-----EALVQEGKARKTNPIQSTLRKLY 240
b 235 ILTVNRKRVATEFESFSLDSTFFAKQIPIVSNLTKEYL 274
RESULT 8
ICE3 MOUSE
ID ICE3 MOUSE STANDARD; PRT; 277 AA.
AC F70677; O08668; Q9QW14;
YT 01-NOV-1997 (Rel. 35, Created)
YT 15-MAR-2004 (Rel. 43, Last sequence update)
YT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-3) (LICE).
EN CASP3 OR CPP32.
DS Mus musculus (Mouse).
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX NCBI_TaxID=10090;
XX [1]
XX SEQUENCE FROM N.A.
XX MEDLINE=96358624; PubMed=8761296;
XX Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
XX Fletcher F.A.;
XX "Molecular characterization of mouse and rat CPP32 beta gene encoding
XX a cysteine protease resembling interleukin-1 beta converting enzyme
XX and CED-3";
XX Oncogene 13:749-755 (1996).
XX [2]
XX SEQUENCE FROM N.A.
XX MEDLINE=97224429; PubMed=9070890;
XX Mukasa T., Urabe K., Momoi M.Y., Kimura I., Momoi T.;
XX "Specific expression of CPP32 in sensory neurons of mouse embryos and
XX activation of CPP32 in the apoptosis induced by a withdrawal of
XX NGF";
XX Biochem. Biophys. Res. Commun. 231:770-774 (1997).
XX [3]
XX SEQUENCE FROM N.A.
XX STRAIN=C3H/An;
XX MEDLINE=97190206; PubMed=9038361;
XX van de Craen M., Vandenberghe P., Declercq W., van den Brande I.,

van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
Piers W.;
RA "Characterization of seven murine caspase family members.";
RA FEBS Lett. 403:61-69 (1997).
[4]
RA SEQUENCE FROM N.A.
RA TISSUE=Brain;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[5]
RA SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary gland;
RA MEDLINE=22388257; PubMed=1247932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udwin T.B., Toshnyki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Vallalao D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Mahting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[6]
RA SEQUENCE OF 58-277 FROM N.A.
RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
RA Fortin J.-P., Sekaly R.-P.;
RA "Multiple pathways of apoptosis converging on the CPP32 protease.";
RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp1-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
CC Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
CC cytokine which is involved in a variety of inflammatory processes.
CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
CC kidney and heart. Lower expression in brain, skeletal muscle and
CC testis.
CC -!- PTM: CLEAVAGE BY GRANTZYME B. CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U54803; AAC52768.1; -;
CC EMBL; U54802; AAC52768.1; JOINED.
CC EMBL; U49929; AAC52764.1; -;

Nat. Struct. Biol. 3:619-625(1996).
[8]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
MEDLINE=97197830; PubMed=9045680;
Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
Priestle J.P., Tomaselli K.J., Gruetter M.G.;
"Structure of recombinant human CPP32 in complex with the
tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
J. Biol. Chem. 272:6539-6547(1997).
[9]
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=20283632; PubMed=10821855;
Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
Levy M.A., Dewolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
"Potent and selective nonpeptide inhibitors of caspases 3 and 7
inhibit apoptosis and maintain cell functionality.";
J. Biol. Chem. 275:16007-16014(2000).
[10]
PROCESSING.
MEDLINE=96353838; PubMed=8755496;
Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
Litwack G., Alnemri E.S.;
"In vitro activation of CPP32 and Mch3 by Mch4, a novel human
apoptotic cysteine protease containing two FADD-like domains.";
Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
[11]
CLEAVAGE OF HUNTINGTIN
MEDLINE=96331283; PubMed=8696339;
Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalcman M.A., Koide H.B.,
Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
Vaillancourt J.P., Hayden M.R.;
"Cleavage of huntingtin by apoptin, a proapoptotic cysteine protease,
is modulated by the polyglutamine tract.";
Nat. Genet. 13:442-449(1996).
[12]
FUNCTION: Involved in the activation cascade of caspases
responsible for apoptosis execution. At the onset of apoptosis it
proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
element binding proteins (SREBPs) between the basic helix-loop-
helix leucine zipper domain and the membrane attachment domain.
Cleaves and activates caspase-6, -7 and -9. Involved in the
cleavage of huntingtin.
[13]
ENZYME REGULATION: Inhibited by isatin sulfonylamides.
[14]
SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
[15]
SUBCELLULAR LOCATION: Cytoplasmic.
[16]
TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
and kidney. Moderate levels in brain and skeletal muscle, and low
in testis. Also found in many cell lines, highest expression in
cells of the immune system.
[17]
PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
AND VICE VERSA.
[18]
SIMILARITY: Belongs to peptidase family C14.

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or send an email to license@isb-sib.ch).

EMBL; U13737; AAA65015.1; -
EMBL; U13738; AAA60355.1; -
EMBL; U26943; AAA74929.1; -

DR EMBL; AJ413269; CAC88866.1; -
DR EMBL; AY219866; AA025654.1; -
DR EMBL; BC016926; AAH16926.1; -
DR PIR; A55315; A55315.
DR PDB; 1PAU; 07-JUL-97.
DR PDB; 1CP3; 24-DEC-97.
DR PDB; 1GFW; 23-JUN-00.
DR MEROPS; C14.003; -
DR Genew; HGNC:1504; CASP3.
DR MIM; 606636; -
DR GO; GO:0004208; F:caspase-3 activity; TAS.
DR GO; GO:000624; P:induction of apoptosis by extracellular sig.; TAS.
DR GO; GO:000829; P:induction of apoptosis by intracellular sig.; TAS.
DR GO; GO:000829; P:induction of apoptosis by intracellular sig.; TAS.
DR GO; GO:000829; P:induction of apoptosis by intracellular sig.; TAS.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR002138; ICE_P10.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
3D-structure. 1 9
FT PROPEP 10 28 APOPAIN P17 SUBUNIT.
FT CHAIN 29 175 APOPAIN P12 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT SITE 121 121 BY SIMILARITY.
FT ACT SITE 163 163 BY SIMILARITY.
FT VARIAT 190 190 D -> E (in isoform beta).
FT CONFLICT 31 36 /FTID=VAR 001401.
FT STRAND 36 36 ISLDSNS -> MSWDNG (IN REF. 3).
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT TURN 67 80
FT HELIX 81 82
FT TURN 81 82
Query Match 22.0%; Score 272.5; DB 1; Length 277;
Best Local Similarity 31.3%; Pred. No. 8.7e-15;
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;
QY 9 EEKYDMSGAALALILCVTK-----AREGSEEDLDALHEMFQRLRFESTMKRDPTA 58
DB 34 DNSYMDYPENGGLCIINNNKFNKSTGTSRGTDVAANLETRNLKYEVNKNLDR 93
QY 59 EQFOBELEKQQAIIDSRDPVSCAFVLLMAHREGFLKGEDG--EMVKLENLFEALNNKN 116
DB 94 EEIVELMRDVSKEHSHKRSFVC---VLLSHGFEGLIFGTNGPVDLKKITNFF---RGDR 147
QY 117 QOALRKPQVYIQAQCGRQDPG-ETVCGDEIVVMVKDPSQTIPTYTDLHVSTVEGY 175
DB 148 CRSTGPKPFIQAQCRGTELDGCIITDSGVDDVAC----HKIPVDADFLVYSTAGY 203
QY 176 IAYRHQKSGSCFIQLVDVFTK--RKGHILELLTEVTRMA-EAEIVQ---EGKARKNPP 229
DB 204 YSWNSKSGSWFICSLCAMLQYADKLEFNMHILTRVNRKVATEFESFDPATFHAQKQIP 263
QY 230 EIQTILKRLY 240
DB 264 CIVSMLTKELY 274
RESULT 10
ICE7 MOUSE
ID ICE7_MOUSE STANDARD; PRT; 303 AA.
AC P97864; O08669;
DT 01-NOV-1997 (Rel. 35, Created)

1 01-NOV-1997 (Rel. 35, Last sequence update)
 2 10-OCT-2003 (Rel. 42, Last annotation update)
 3 Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
 4 protease Mch-3).
 5 CASP7 OR MCH3 OR LICE2.
 6 Mus musculus (Mouse).
 7 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 8 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 9 MCB_TaxID=10090;
 10 [1]
 11 SEQUENCE FROM N.A.
 12 TISSUE=Skeletal muscle;
 13 MEDLINE=97224489; PubMed=9070923;
 14 Juan T.S.-C., McNelece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 15 Copeland N.G., Fletcher F.A.;
 16 "Identification and mapping of Casp7, a cysteine protease resembling
 17 CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 18 Genomics 40:86-93(1997).
 19 [2]
 20 SEQUENCE FROM N.A.
 21 MEDLINE=97236307; PubMed=91251129;
 22 Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
 23 Momoi T.;
 24 "Wormamin enhances CPP32-like activity during neuronal
 25 differentiation of P19 embryonal carcinoma cells induced by retinoic
 26 acid.";
 27 T Biochem. Biophys. Res. Commun. 232:192-197(1997).
 28 [3]
 29 SEQUENCE FROM N.A.
 30 STRAIN=C3H/An;
 31 MEDLINE=97190206; PubMed=9038361;
 32 van de Craen M., Vandenaebale P., Declercq W., van den Brande I.,
 33 van de Craen M., Moelens P., Schotte P., van Crielinge W., Beyaert R.,
 34 Fiers W.;
 35 "Characterization of seven murine caspase family members.";
 36 FEBS Lett. 403:61-69(1997).
 37 [4]
 38 SEQUENCE FROM N.A.
 39 MEDLINE=2238257; PubMed=12477932;
 40 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 41 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 42 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 43 Hopkins R.F., Jordan H., Moore S.I., Wang J., Wang J., Hsieh F.,
 44 Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 45 Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 46 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
 47 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 48 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 49 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 50 Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 51 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 52 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 53 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 54 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 55 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 56 "Generation and initial analysis of more than 15,000 full-length
 57 human and mouse cDNA sequences.";
 58 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 59 [1-] FUNCTION: Involved in the activation cascade of caspases
 60 responsible for apoptosis execution. Cleaves and activates sterol
 61 regulatory element binding proteins (SREBPs). Overexpression
 62 promotes programmed cell death (By similarity).
 63 [1-] SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
 64 [1-] SUBCELLULAR LOCATION: Cytoplasmic.
 65 [1-] TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
 66 KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
 67 EXPRESSION IN THE BRAIN.
 68 [1-] PM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 69 SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 70 CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 71 CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 72 VICE VERSA (BY SIMILARITY).

CC -1- SIMILARITY: Belongs to peptidase family C14.
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 CC -----
 DR EMBL; U67321; AAC53068.1; ALT_INIT.
 DR EMBL; D86353; BAA19730.1; -.
 DR EMBL; Y13088; CAA73530.1; -.
 DR EMBL; BC005428; AAH05428.1; -.
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.004; -.
 DR MGD; MGI:109383; Casp7.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PRO0376; ILIBCENZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS02027; CASPASE_P10; 1.
 DR PROSITE; PS02028; CASPASE_P20; 1.
 DR Hydrolase; Thiol protease; Zymogen; Apoptosis.
 KW PROPEP 1 23
 FT CHAIN 24 198
 FT PROPEP 199 206
 FT CHAIN 207 303
 FT ACT_SITE 144 144
 FT ACT_SITE 186 186
 FT CONFLICT 10 11
 FT CONFLICT 45 45
 FT CONFLICT 48 49
 FT SEQUENCE 303 AA; 34060 MW; 747787B5BDE5F744 CRC64;
 SQ
 Query Match 21.8%; Score 270; DB 1; Length 303;
 Best Local Similarity 32.6%; Pred. No. 1.5e-14;
 Matches 71; Conservative 36; Mismatches 101; Indels 10; Gaps 4;
 QY 29 REGSEEDLDALHMFRLPSTMKRDPPTABQFOEILEKFOQAIDSRSDVSCAFVVLMA 88
 Db 87 RGTGDKDAGALFKCFQNLGFVTVHDCSCAKMDLLRKASEEDHSNS---ACFACVLLS 143
 QY 89 HGREGFLKGEDCEMYKLENFEALNNKNCQALRAKPKVYIIQACRGQRDPGETVGGDEI 148
 Db 144 HGEEDLIYKGG-VTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDGQADSGPI 202
 QY 149 VNVIKDSPQTPTTYTDALHVTSTVEGYIARHDKGSCFIQTLDVDFVK--RKHILELL 206
 Db 203 NIDANPRNKIPVEADFLFAYSTVGYVWENPGKSGWFVQALCSILNKGKXLEIMQIL 262
 QY 207 TEVTRMAAEVLQGGKAR-----KTNPEIQSTLRKLY 240
 Db 263 TRVNDRVARHFESQSDDPFRFNEKQIQPCMVSMLTKEYL 300
 RESULT 11
 ICE7_MESAU
 ID ICE7_MESAU STANDARD; PRT; 303 AA.
 AC P55214;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
 DE (SCA-2).
 DE CASP7 OR MCH3.
 GN Mesocricetus auratus (Golden hamster).
 OS Mesocricetus auratus; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
NCBI_TaxID=10036;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=SYRIAN; TISSUE=Liver;
MEDLINE=96224303; PubMed=8643593;
Pai J.-T., Brown M.S., Goldstein J.L.;
"Purification and cDNA cloning of a second apoptosis-related cysteine
protease that cleaves and activates sterol regulatory element binding
proteins.";
Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
C -I- FUNCTION: Involved in the activation cascade of caspases
responsible for apoptosis execution. Cleaves and activates sterol
regulatory element binding proteins (SREBPs). Proteolytically
cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
bond. Overexpression promotes programmed cell death (by
similarity).
C -I- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
(By similarity).
C -I- SUBCELLULAR LOCATION: Cytoplasmic.
C -I- PM: CLEAVAGES BY GRANTZYM B OR CASPASE-10 GENERATE THE TWO ACTIVE
SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
VICE VERSA (BY SIMILARITY).
C -I- SIMILARITY: Belongs to peptidase family C14.

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EMBL: U47332; AAC52595.1; --
HSP: P42574; LPAU.
MEROPS: C14.004; --
InterPro: IPR002138; ICE_P10.
InterPro: IPR001309; ICE_P20.
InterPro: IPR002398; Peptidase C14.
Pfam: PF00656; Peptidase C14; 1.
PRINTS: PR00376; ILIBENZYM.
SMART: SM0115; CASC; 1.
PROSITE: PS01122; CASPASE_CYS; 1.
PROSITE: PS01121; CASPASE_HIS; 1.
PROSITE: PS0207; CASPASE_P10; 1.
PROSITE: PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Apoptosis.
PROPEP 1 23 CASPASE-7 SUBUNIT P20.
CHAIN 24 198 BY SIMILARITY.
PROPEP 199 206 CASPASE-7 SUBUNIT P11.
CHAIN 207 303 BY SIMILARITY.
ACT SITE 144 144 BY SIMILARITY.
ACT SITE 186 186 BY SIMILARITY.
SEQUENCE 303 AA; EA29356D90984648 CRC64;
Query March 21:08; Score 260; DB 1; Length 303;
Best Local Similarity 31.7%; Pred. No. 9.8e-14;
Matches 69; Conservative 39; Mismatches 100; Indels 10; Gaps 5;
Y 29 REGSEEDLALHFRQLRPFSTMKRPTAEQFQEELEKFOQAIDSRDPVSCAFVILMA 88
D 87 RGTGDKDAELFKFRSGFDGVVYVNDSCAKQDLLRKASEBDHNS---ACFACVLLS 143
Y 89 HGRGFLKGEDEMGVLENLFEALNNKNCALAKPKVYIQAACRQDPGETVGGDEI 148
D 144 HGEENLYKDG-VTPIDTAFHFRGDRCKTLLKPKLFFIQACRGTLEDGQVADSGPI 202
Y 149 VMWIKDSQTIPTVTDALHYSTVEGVIAVRHPQKSGCSFTQTLVDVFTK--RGHILELL 206
D 203 NETDANPKYLPVZADFLPAYSTVPGYVSNFCKGSFWQALCSILDEHGKDLIEWQL 262

QY 207 TEVTRMA--EALVQB-GKARKTNPEIOSTLKRLY 240
DB 263 TRVDRVARHFESQCDPCFNEKQIPCMVSMILKELY 300
RESULT 12
ICE7 HUMAN
ID ICE7 HUMAN STANDARD; PRT; 303 AA.
AC P55210; Q13364; Q96BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (CWH-1).
GN CASP7 OR MCH3
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Placentalia; Primates; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=96139498; PubMed=8576161;
RX Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
RX Dixit V.M.;
RA "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
cell death protein Ced-3 is activated during Fas- and tumor necrosis
factor-induced apoptosis.";
RT J. Biol. Chem. 271:1621-1625(1996).
RL [2]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
RN TISSUE=Spleen;
RX MEDLINE=96147144; PubMed=8567622;
RX Lippke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
RA "Identification and characterization of CPP32/Mch2 homolog 1, a novel
cysteine protease similar to CPP32.";
RT J. Biol. Chem. 271:1825-1828(1996).
RL [3]
SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RN TISSUE=T-cell;
RX MEDLINE=96105019; PubMed=8521391;
RX Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
RX Fritze L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salveson G.,
RX Earnshaw W.C., Litwack G., Alnemri E.S.;
RA "Mch3, a novel human apoptotic cysteine protease highly related to
CPP32.";
RT Cancer Res. 55:6045-6052(1995).
RL [4]
SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
RN TISSUE=Fetal lung, and fetal spleen;
RX MEDLINE=97224489; PubMed=9070923;
RX Juan T.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RX Copeland N.G., Fletcher F.A.;
RA "Identification and mapping of Casp7, a cysteine protease resembling
CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RX Genomics 40:86-93(1997).
RN [5]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
RN TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RX Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RX Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RX Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

PROCESSING.

MEDLINE=96353838; PubMed=8755496; Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J., Litwack G., Alnemri E.S., "In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains," Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).

-!- FUNCTION: Involved in the activation cascade of caspases responsible for apoptosis execution. Cleaves and activates sterol regulatory element binding proteins (SREBPs). Proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217 bond. Overexpression promotes programmed cell death.

-!- ENZYME REGULATION: Inhibited by isatin sulfonamides.

-!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3; Name=Alpha; IsoId=P55210-1; Sequence=Displayed; Name=Beta; IsoId=P55210-2; Sequence=VSP_000807; Note=Not proteolytically active; Name=Alpha; Synonyms=Beta; IsoId=P55210-3; Sequence=VSP_000806; Note=What we call isoform Alpha' is known in Ref.4 as Beta; TISSUE SPECIFICITY: Highly expressed in lung, skeletal muscle, liver, kidney, spleen and heart, and moderately in testis. No expression in the brain.

-!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND VICE VERSA.

-!- SIMILARITY: Belongs to peptidase family C14.

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EMBL; U39613; AAC50346.1; -
EMBL; U40281; AAC50352.1; -
EMBL; U37448; AAC50303.1; -
EMBL; U37449; AAC50304.1; -
EMBL; U67319; AAC51152.1; -
EMBL; U67320; AAC51153.1; -
EMBL; U67206; AAF21460.1; -
EMBL; BC015799; AAH15799.1; -
PDB; 1FLJ; 23-MAY-01.
PDB; 1GQF; 04-JAN-02.
PDB; 1I40; 31-OCT-01.
PDB; 1I51; 23-FEB-02.
PDB; 1K86; 21-NOV-01.
PDB; 1K88; 21-NOV-01.
PDB; 1KMC; 16-JAN-02.
MEROPS; C14.004; -
Genew; HGNC:1508; CASP7.
MIM; 601761; -
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0008234; F:cysteine-type peptidase activity; TAS.
GO; GO:0008632; P:apoptotic program; TAS.

DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; IILBCEZYME.
DR SMART; SMO0115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW 3D-structure.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186
FT VARSPLIC 1 1 M-> MDCVWPGRKWHLEKNTSCGSSGICASYVTQM (in isoform Alpha').
FT VARSPLIC 149 303 /FTID=VSP_000806.
FT ELDDGIQADSGPINDANPKYKIPVEADFLFAYSTVPGY
FT SWRSGSGSWFVALCSILEHKGKLEIMQILTRVNDVAR
FT HTSQSDHDFHFKKQIPCVWSMLTKELVFSO -> MESCS
FT VTQGVORRLGLQPPPPRLAEGPSLIMWASRTRGSMTO
FT MLILDTRSQMKLTSSSPFPFQAITRGGAQEAPGLCKPSA
FT PSWRSTKTKWKSRSRSPG (in isoform Beta).
FT /FTID=VSP_000807.
FT MUTAGEN 186 186 C->A: NO APOPTOTIC ACTIVITY.
FT CONFLICT 4 4 D -> E (IN REF. 5).
FT CONFLICT 194 194 G -> A (IN REF. 1).
FT SEQUENCE 303 AA; 34276 MW; CD373EE54A232CA4 CRC64;
Query Match 20.7%; Score 256; DB 1; Length 303;
Best Local Similarity 30.7%; Pred. No. 2e-13;
Matches 67; Conservative 39; Mismatches 102; Indels 10; Gaps 4;
QY 29 REGSEEDLDLEHMFROLRPESTWKRPTAEQFOEELEKFOQALDSREDVSCAFVVLMA 88
DB 87 RNGTHDKDAELFKFRSLGDFVIYVNDSCAKMDLLK---ASEEDTNAAACFACILLS 143
QY 89 HGREGLKGEDGEMVKLENLEALNNKNCQALRAKPKVYIQCRGEQRDPGTGVGDEI 148
DB 144 HGEENVYKDG-VTPIKDLTAHFRGDRCKTLLEKPKLFTIQACRGTELDGDIQADSGPI 202
QY 149 VMVVKDSQTTPTVTDALHYVSTVEGYIAYEHDKGSCFTQTLVDVFTK--RKGHILELL 206
DB 203 NDTDANPKYKIPVEADFLFAYSTVPGYSWRSPGSGSWFVQALCSILEHKGKLEIMQIL 262
QY 207 TEVTRMAEALVQBG-----KARKTNPSIQSTLRKRLY 240
DB 263 TVNDRVARHFTESQSDPHFHEKKQIPCVWSMLTKELY 300
RESULT 13
CED3_CABEL
ID CED3_CABEL STANDARD; PRT; 503 AA.
AC P42573; P45435; Q9GQO4; Q9NAQ8;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cell death protein 3 precursor (EC 3.4.22.-).
GN CED-3 OR C48D1.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC STRAIN=Bristol N2;
RX MEDLINE=94061982; PubMed=8242740;
RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;

A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,
 A Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 A Liu K., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 A Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 A Palazolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
 A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 A Shue B.C., Siden-Kiamis I., Simpson M., Skupski M.P., Smith T.,
 A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 A Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 A Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 A Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 I "The genome sequence of *Drosophila melanogaster*."
 L Science 287:2185-2195 (2000).
 [3]
 P SEQUENCE FROM N.A.
 C STRAIN=Berkeley; TISSUE=Head;
 C MEDLINE=22426066; PubMed=12537569;
 X A Stapleton M., Carlson J.W., Brakstein P., Yu C., Champe M.,
 A George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 A Rubin G.M., Celnik S.E.,
 T "A *Drosophila* full-length cDNA resource."
 L Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
 C C -i- FUNCTION: Involved in the activation cascade of caspases
 C responsible for apoptosis execution. Acts downstream of rpr.
 C cleaves baculovirus p35 and lamin Dmo in vitro.
 C -i- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
 C -i- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
 C occurs.
 C -i- SIMILARITY: Belongs to peptidase family C14.
 C -----
 C This SWISS-PROT entry is copyright. It is produced through a collaboration
 C between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 C -----
 C EMBL: Y12261; CA72937.1; --
 C EMBL: AE003771; AF56339.1; --
 C EMBL: AY058451; AL113680.1; --
 C HSSP: P42574; 1PAU.
 C MEROPS: C14.015; --
 C FlyBase: FBgn0019972; Ice.
 C GO: GO:0004207; P:effector caspase activity; NAS.
 C GO: GO:0006915; P:apoptosis; NAS.
 C GO: GO:0006915; P:apoptosis; NAS.
 C InterPro: IPR002136; ICE_P10.
 C InterPro: IPR001309; ICE_P20.
 C InterPro: IPR002398; Peptidase C14.
 C Pfam: PF00656; Peptidase C14; 1.
 C PRINTS: PR00376; I11BCEZYME.
 C SMART: SM00115; CASP; 1.
 C PROSITE: PS01122; CASPASE_CYS; 1.
 C PROSITE: PS01122; CASPASE_HIS; 1.
 C PROSITE: PS02070; CASPASE_P10; 1.
 C PROSITE: PS02070; CASPASE_P20; 1.
 C PROSITE: PS02070; CASPASE_P20; 1.
 C Hydrolase; Thiol protease; Zymogen; Apoptosis.
 C PROPEP 1 28 BY SIMILARITY.
 C CHAIN 29 217 CASPASE SUBUNIT P21 (BY SIMILARITY).
 C PROPEP 218 230 BY SIMILARITY.
 C CHAIN 231 339 CASPASE SUBUNIT P12 (BY SIMILARITY).
 C ACT_SITE 169 169 BY SIMILARITY.
 C ACT_SITE 211 211 BY SIMILARITY.
 C CONFLICT 151 151 A -> S (IN REF. 1).
 C CONFLICT 265 265 S -> T (IN REF. 1).
 C SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;

Query Match 20.0%; Score 247.5; DB 1; Length 339;
 Best Local Similarity 30.5%; Pred. No. 1.1e-12;
 Matches 60; Conservative 42; Mismatches 76; Indels 19; Gaps 5;
 QY 27 KARGSEEDLDALHEMFROLRFESTMKRDPFAFOBELEKFOCAIDSDREDPVSCAFVVL 86
 DB 110 KSRAGTNVDCNLTURLVKQDFFETVTKDC--YYKDLILATIEYASQNSHSDCILVAL 166
 QY 87 MAHGREGLKEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGQRDPGETV--- 143
 DB 167 LSHGEMGIYAKDTQ-YKLDNINWFFFTANHCPSLAGPKLFFIQAQCGRLDGGVTMQRS 225
 QY 144 ----GGEIVNVKDSQTFITYTDALHVTSTVEGYAYEHDKGSCFICQLVDVFTK-- 197
 DB 226 QTEITDGD-----SSMSYKIPVHADFLIAYSTVPGFYSWENTTRGWSFWMSLCALAAANG 279
 QY 198 RKGHILELLTEVTERMA 214
 DB 280 KELDILTLTLTFVCORVA 296
 RESULT 15
 IC88 HUMAN
 ID IC88 HUMAN STANDARD; PRT; 479 AA.
 AC Q14790; Q14676; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796;
 AC Q15780; Q15806; Q8TD11; Q8TD12; Q8TD13; Q8TD14; Q8TD15; Q96T22;
 AC Q9COK4; Q9UQ81;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
 DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
 DE like protease) (FADD-like ICE) (ELICE) (Apoptotic cysteine protease)
 DE (Apoptotic protease Mch-5) (CAP4).
 GN CASP8 OR MCH5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).
 RC TISSUE=B-cell and Thymus;
 RX MEDLINE=96279826; PubMed=8681376;
 RA Boldin M.P., Goncharov T.M., Goitsev Y.V., Wallach D.;
 RA "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
 RT Fas/APO-1- and TNF receptor-induced cell death.";
 RL Cell 85:803-815 (1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
 RX MEDLINE=96279827; PubMed=8681377;
 RA Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
 RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
 RA Krammer P.H., Peter M.E., Dixit V.M.;
 RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
 RT to the CD95 (Fas/APO-1) death-inducing signaling complex.";
 RL Cell 85:817-827 (1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=T-cell;
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99132295; PubMed=9931493;
 RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
 RT "Structure and chromosome localization of the human CASP8 gene.";
 RL Gene 226:225-232 (1999).

[5] P SEQUENCE FROM N.A. (ISOFORM 2).
X MEDLINE=97373543; PubMed=9228018;
A Strinivasula S.M., Ahmad M., Ohtsuka S., Bullrich F., Banks S.,
A Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
A Armstrong R.C., Alnemri E.S.;
T "FLAME-1, a novel PADD-like anti-apoptotic molecule that regulates
L Fas/TNFR1-induced apoptosis";
L J. Biol. Chem. 272:18542-18545 (1997).
[6] P SEQUENCE FROM N.A.
X MEDLINE=21100893; PubMed=11161814;
A Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
A Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
A Ikeda J.-E., Hayden M.R.;
T "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
T and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2),
T critical region at chromosome 2q33-q34: candidate genes for ALS2";
L Genomics 71:200-213 (2001).
[7] P SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
C TISSUE=Leukocyte;
P MEDLINE=22005982; PubMed=12010809;
X Hameji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
A Harada M.;
T "Characterization of caspase-8L: a novel isoform of caspase-8 that
T behaves as an inhibitor of the caspase cascade";
L Blood 99:4070-4078 (2002).
[8] P SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9
N WITH SCAP3 AT THE ENDOPLASMIC RETICULUM.
P MEDLINE=21927603; PubMed=11917123;
X Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;
P "The procaspase-8 isoform, procaspase-8L, recruited to the BAP3
T complex at the endoplasmic reticulum";
L Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336 (2002).
[9] P SEQUENCE FROM N.A. (ISOFORM 7).
C TISSUE=Leukocyte;
P MEDLINE=22388257; PubMed=12477932;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
A Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
A Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
A Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length
T human and mouse cDNA sequences";
L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[10] P PARTIAL SEQUENCE, AND PROCESSING.
X MEDLINE=97121412; PubMed=8962078;
X Strinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
A Alnemri E.S.;
T "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
T protease Mch5 is a CrmA-inhibitable protease that activates multiple
T Ced-3/ICE-like cysteine proteases";
L Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
[11] P FUNCTION.
X MEDLINE=97160607; PubMed=9006941;
X Muzio M., Salvesen G.S., Dixit V.M.;
T "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
T zymogens";
L J. Biol. Chem. 272:2952-2956 (1997).
[12] P PROCESSING.
X MEDLINE=97327557; PubMed=9184224;
A Medema J.P., Scalfi C., Kischkel F.C., Shevchenko A., Mann M.,
A Krammer P.H., Peter M.E.;
T "FLICE is activated by association with the CD95 death-inducing
T signaling complex (DISC)";
L EMBO J. 16:2794-2804 (1997).
[13] P CHARACTERIZATION OF ISOFORM 7.
X MEDLINE=20318377; PubMed=10860845;
A Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
A Hayashi K.;
T "Dominant expression of a novel splice variant of caspase-8 in human
T peripheral blood lymphocytes";
L Biochem. Biophys. Res. Commun. 272:877-881 (2000).
[14] P INTERACTION WITH BCL2; BCL2L1 AND BCAP31.
X MEDLINE=97477382; PubMed=9334338;
X Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
A Cromlish J.A., Shore G.C.;
T "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
T endoplasmic reticulum";
L J. Cell Biol. 139:327-338 (1997).
[15] P INTERACTION WITH PEAL5.
X MEDLINE=99369240; PubMed=10442631;
X Condorelli G., Vigliotta G., Caffieri A., Trencia A., Andalo P.,
A Oriente P., Miele C., Caruso M., Formisano P., Beguinot F.;
T "PBD/PEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
T induced apoptosis";
L Oncogene 18:4409-4415 (1999).
[16] P X-RAY CRYSTALLOGRAPHY (2.8 ÅNGSTRÖMS).
X MEDLINE=99451259; PubMed=10508784;
X Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
A Wu J.C., Tonaselli K.J., Gruetter M.G.;
T "The three-dimensional structure of caspase-8: an initiator enzyme in
T apoptosis";
L Structure 7:1125-1133 (1999).
[17] P VARIANT CASP8 TRP-248.
X MEDLINE=22399940; PubMed=12353035;
X Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
A Dale J.K., Fack J., Davis J., Hall C.G., Skoda-Smith S.,
A Atkinson T.P., Straus S.B., Lenardo M.J.;
T "Pleiotropic defects in lymphocyte activation caused by caspase-8
T mutations lead to human immunodeficiency";
L Nature 419:395-399 (2002).
-!- FUNCTION: Most upstream protease of the activation cascade of
C caspases responsible for the TNFRSF6/Fas mediated and TNFRSF1A
C induced cell death. Binding to the adapter molecule FADD recruits
C it to either receptor. The resulting aggregate called death-
C inducing signaling complex (DISC) performs CASP8 proteolytic
C activation. The active dimeric enzyme is then liberated from the
C DISC and free to activate downstream apoptotic proteases.
C Proteolytic fragments of the N-terminal propeptide (termed CAP3,
C CAP5 and CAP6) are likely retained in the DISC. Cleaves and
C activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
C participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
C Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
C Likely target for the cowpox virus CRMA death inhibitory protein.
C Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
C with the pro-apoptotic activity of the complex.
-!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
C Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
C endoplasmic reticulum with a complex containing BCAP31, BAP29,
C BCL2 and/or BCL2L1.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:

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[ ] Event=Alternative splicing; Named isoforms=9;
[ ] Name=1; Synonyms=Alpha-1;
[ ] IsoId=Q14790-1; Sequence=Displayed;
[ ] Name=2; Synonyms=Alpha-2, MCH5-beta;
[ ] IsoId=Q14790-2; Sequence=VSP_000810;

Query Match      19.9%; Score 246.5; DB 1; Length 479;
Best Local Similarity 29.7%; Pred No. 2,1e-12;
Matches 80; Conservative 37; Mismatches 115; Indels 37; Gaps 9;

Y   3  NPRSLEEEK-----YDMGGAALAILCV-----TKARE-----GSEEDLDAL 39
C   211 SPREQDSEQTLDKVYQMKSPRGYCLIIINNHNFAKAREKVPKLHSIRDRNGTHLDAGAL 270
Y   40 EHMFCRLREESTMKDPTAEQFQBELEKFOQAIDSRDPVSCAFVWLMARGEGFLKGED 99
b   271 TTTFEELHFEIKPHDDCTVEQIYEILKIYQLMDHSNMD---CFICCLSHGDKGIYGTD 327
Y   100 GEMVKLENLFEALNNKNCOALRAKPKVYIIQACRGEQRDPGETVGGDE----IVMVIKDS 155
b   328 GQEAPIVELTSQFTGLKCPSLAGKPKVFIIQACQGDNYQKGIPIVETDSEEQPVLEMDLSS 387
Y   156 PQT--IPTYTDALHYVSTVEGYIAYEHQKGSCTFIQTLDVDFTKR--KG-HILELLTEVT 210
b   388 PQTRYIPDEADFLLGWATVNNCVFNPAEGTWIQLCSLRERCPRGDDILTILTEVN 447
Y   211 RRMAEAEVLQEGKARKTNPEIQSTLRKEL 239
b   448 YEVSNKD--DKKMGKQMPQPTFTLRKXL 474
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earch completed: March 19, 2004, 11:22:46
ob time : 10.6414 secs

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WM protein - protein search, using sw model

Run on: March 19, 2004, 11:18:31 ; Search time 13.498 Seconds
(without alignments)
1724.577 Million cell updates/sec

Title: US-09-989-903-5

Perfect score: 1239

Sequence: 1 MSNPRSLSEEEKYDMSGALAL.....KARKTNPEIQSTLRRLYLQ 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	2 JC7517	caspase-14/a - human
2	293	23.6	452	2 JC6507	caspase-2 - rat
3	289	23.3	435	2 A54821	apoptosis regulato
4	282.5	22.8	277	2 JC5410	CPP32 protein - mo
5	280.5	22.6	277	2 S64710	cysteine proteinas
6	272.5	22.0	277	2 A53315	cysteine proteinas
7	264.5	21.3	454	2 JC7123	caspase-9 long cha
8	248.5	20.1	503	2 A49429	interleukin-1 beta
9	246.5	19.9	212	2 I67437	cysteine proteinas
10	239.5	19.3	416	2 G02635	ICE-LAP6 - human
11	230	18.6	495	2 T20038	hypothetical prote
12	226	18.2	311	2 B56084	interleukin-1 beta
13	226	18.2	383	2 A56084	interleukin-1 beta
14	226	18.2	404	2 A42677	interleukin-1 beta
15	225	18.2	418	2 B57511	interleukin-1 beta
16	217.5	17.6	402	2 A64495	IL-1 beta converta
17	213.5	17.2	182	2 I67436	interleukin-1 beta
18	210.5	17.0	826	2 T43638	caspase-related pr
19	207	16.7	263	2 C56084	interleukin-1 beta
20	205.5	16.6	377	2 A57511	interleukin-1 beta
21	197	15.9	312	2 B54821	apoptosis regulato
22	189	15.3	536	2 T43633	caspase-related pr
23	185	14.9	488	2 T13385	hypothetical prote
24	174.5	14.1	642	2 T27021	hypothetical prote
25	159.5	12.9	136	2 I53300	interleukin-1 beta
26	103.5	8.4	1313	2 A48467	myosin heavy chain
27	98	7.9	1357	2 A45627	caspase protein 3
28	97.5	7.9	139	2 T43642	caspase protein 3
29	97	7.8	1051	2 T18302	ap5 protein - Eme

chromosome segrega
myosin-3 heavy cha
chemotaxis protei
hypothetical prote
ER-golgi intermedi
recombination prot
L-fucose kinase
rhamnulokinase (EC
chromokinesin - ch
probable flagellar
caspase protein 1C
excinuclease ABC 8
neural cell adhesi
chromosomal protei
kinesin-related pr
H+-transporting tw

30 95.5 7.7 1190 2 E84193
31 95.5 7.7 2104 2 T38774
32 95 7.7 761 2 E82205
33 91 7.3 394 2 T25968
34 91 7.3 510 2 S42626
35 90.5 7.3 520 2 F70350
36 89.5 7.2 467 2 D95253
37 89.5 7.2 482 2 B98118
38 89.5 7.2 1225 2 A56514
39 89 7.2 352 2 G71328
40 88.5 7.1 149 2 T43637
41 88.5 7.1 661 2 B97733
42 88.5 7.1 858 1 IJRTNC
43 88.5 7.1 1203 2 B55094
44 88.5 7.1 2954 2 T14156
45 88 7.1 505 2 S39520

RESULT 1
JC7517
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7517
R: Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.
Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A: Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte
A: Reference number: JC7517; MUID: 20517231; PMID: 11062009
A: Contents: Epidermal keratinocytes
A: Accession: JC7517
A: Molecule type: mRNA
A: Residues: 1-242 <ECK>
A: Cross-references: GB: AF097874
C: Comment: This enzyme accumulates during keratinocyte differentiation and is activated
C: Genetics:
A: Gene: casp-14/a
A: Map position: 19p13.1
A: Introns: 9/3; 59/3; 135/1; 174/1; 208/3
C: Keywords: differentiation

Query Match 99.6%; Score 1234; DB 2; Length 242;
Best Local Similarity 99.6%; Pred. No. 1.2e-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFQRLRFESTWKRDPDTAQ 60
Db 1 MSNPRSLSEEEKYDMSGARLALLCVTKAREGSEEDLDALHEMFQRLRFESTWKRDPDTAQ 60
QY 61 FOEELEKFOQAIDSDREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
Db 61 FOEELEKFOQAIDSDREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQDPGETVGGDSIVNVVIKDSPTIPTYTDALHVTSTVEGYAYRH 180
Db 121 RAKPKVYIIQACRGQDPGETVGGDSIVNVVIKDSPTIPTYTDALHVTSTVEGYAYRH 180
QY 181 DOKSGCFIQTLLVDVFTTKRGHILELLTEVTRMAEALVOEGKARKTNPEIQSTLRKLY 240
Db 181 DOKSGCFIQTLLVDVFTTKRGHILELLTEVTRMAEALVOEGKARKTNPEIQSTLRKLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 2
JC6507
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

ALIGNMENTS


```
;Accession: JC6507
;Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
;Date: 127-132, 1997
;Title: Cloning and expression of the cDNA encoding rat caspase-2.
;Reference number: JC6507; MUID:98087427; PMID:9427555
;Accession: JC6507
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-452 <SAT>
;Cross-references: GB:U77933; NID:g2769705; PIDN:AAB963379.1; PID:g2769706

Query Match      23.6%; Score 293; DB 2; Length 452;
Best Local Similarity 31.5%; Pred. No. 3e-15; Indels 36; Gaps 7;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Y 29 REGSEEDLDALHMFQRLFEFTMKRDPPTAEQFQEELEKFOQAIDSRDPVSCAFVILMA 88
b 219 RSGGDVHTTTLVTKLLGVNVHVLVDQTAQEMQEKLNFAQ-LPAHRVTDSC-IVALLS 276
Y 89 HGREGLKGEDGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
b 277 HGVEGGIYGVGKLLQQLQVFLFDNANCPSLQNKPKMFFQACRGEDETRGVQQDGKN 336
Y 141 -----ETVGGDEIVMWIKDSPQTIPTTIDALHYVSTVEGYIAYRHDKGSCFIOTLV 192
b 337 HAQSPGCEESDAGKEELMKVR-----LPTSDMIGYACLGKNAAMRNKRGSWYIEALT 391
Y 193 DVFTKR--KGHILELLETVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
b 392 QVFSEACDMHVDMLVKVNALIKE-----REGVAPGTEPHRCSEMSEYCSILCOOLYL 445

RESULT 3
154821
;Species: Homo sapiens (man)
;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
;Accession: A54821
;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
;Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
;Reference number: A54821; MUID:94373811; PMID:8067842
;Accession: A54821
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-435 <WAN>
;Cross-references: GB:U13021; NID:g537291; PID:g537292
;Keywords: alternative splicing; apoptosis

Query Match      23.3%; Score 289; DB 2; Length 435;
Best Local Similarity 31.1%; Pred. No. 5.9e-15; Indels 36; Gaps 7;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

Y 29 REGSEEDLDALHMFQRLFEFTMKRDPPTAEQFQEELEKFOQAIDSRDPVSCAFVILMA 88
b 202 RSGGDVHSTLTLVTKLLGVNVHVLVDQTAQEMQEKLNFAQ-LPAHRVTDSC-IVALLS 259
Y 89 HGREGLKGEDGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
b 260 HGVEGGIYGVGKLLQQLQVFLFDNANCPSLQNKPKMFFQACRGEDETRGVQQDGKN 319
Y 141 -----ETVGGDEIVMWIKDSPQTIPTTIDALHYVSTVEGYIAYRHDKGSCFIOTLV 192
b 320 HAGSPGCEESDAGKE-----KLPGWRLPTSDMIGYACLGKNAAMRNKRGSWYIEALA 374
Y 193 DVFTKR--KGHILELLETVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
b 375 QVFSEACDMHVDMLVKVNALIKD-----REGVAPGTEPHRCSEMSEYCSILCOOLYL 428

RESULT 4
JC5410
;Species: Mus musculus (house mouse)
;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
;Accession: JC5410
;Mukasa, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
;Biochem. Biophys. Res. Commun. 231, 770-774, 1997
;Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
;Reference number: JC5410; MUID:97224429; PMID:9070890
;Accession: JC5410
;Status: nucleic acid sequence not shown
;Molecule type: mRNA
;Residues: 1-277 <MUK>
;Cross-references: DDBJ:D86352
;Experimental source: embryo
;Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match      22.8%; Score 282.5; DB 2; Length 277;
Best Local Similarity 32.4%; Pred. No. 1.1e-14; Indels 27; Gaps 8;
Matches 81; Conservative 38; Mismatches 104; Indels 27; Gaps 8;

QY 9 BEKYDMSGAAALALILCVT-----KAREGSEEDLDALHMFQRLFEFTMKRDPPTA 58
Db 34 DSSYKWDYPENGICIIINKNFKHSTGTGWSRSRGTVDAAANLRETFMGLKYEVNRKNDLTR 93
QY 59 EQFQEELEKFOQAIDSRDPVSCAFVILMAHGREGLKGEDGMVKLENLFEALNNKNCQ 118
Db 94 EEIMELMDSVSKEDSHKSSSFVC---VILSHGDEGVIFGNGP-VDLKLTSPFRGDCR 149
QY 119 ALRAKPKVYIIQACRGEQDPG-ETVGGDEIVMWIKDSPQTIPTTIDALHYVSTVEGYIA 177
Db 150 SLTGKPKFLIIQACRGTDLDCGIETDSTDEMAC---QKIPVEADFLYAYSTAPGYYS 205
QY 178 YRHDKGSCFIOTLVDFVTKRKGHILE---LLTEVTRMA-----EALVQEGKARKTNPE 230
Db 206 WRNSKDGSWFIQSLCSML-KLYAHKLEFHLTRVNRKVATEPESFSLDSTFFHAKKQIPC 264
QY 231 IOSTLRKRLYL 240
Db 265 IVSMLTKELY 274

RESULT 5
S64710
;Species: Cricetus griseus (Chinese hamster)
;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
;Accession: S64710; S72395
;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
;EMBO J. 15, 1012-1020, 1996
;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
;Reference number: S64710; MUID:96183185; PMID:8605870
;Accession: S64710
;Status: nucleic acid sequence not shown
;Molecule type: mRNA
;Residues: 1-277 <WAN>
;Cross-references: EMBL:U27463
;Wang, X.
submitted to the EMBL Data Library, May 1995
;Accession: S72395
;Reference number: S72395
;Molecule type: mRNA
;Residues: 1-79, A, 81-146, Y, 148-277 <WAW>
;Cross-references: EMBL:U27463; NID:G1244443; PIDN:AAB01511.1; PID:G1244444
;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match      22.6%; Score 280.5; DB 2; Length 277;
Best Local Similarity 35.9%; Pred. No. 1.6e-14; Indels 17; Gaps 7;
Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;

QY 29 REGSEEDLDALHMFQRLFEFTMKRDPPTAEQFQEELEKFOQAIDSRDPVSCAFVILMA 88
Db 64 RSGTVDAAKLRFTFMNLKYEVNRKNDLTRFEEIVELMKVNASKEDSHKSSSFVC---VILS 120
QY 89 HGREGLKGEDGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG-ETVGGDE 147
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121 HGDEGVFGDGP-IDLKLTSTVFRGDRSRSLGKPKLFIQACRGTELDGCIETDSSTE 179
148 IVMVVKDSPTIYTDALHVVSTVEGYIAYRHQKQSCFIQTLVDVFTPKRGHILE--- 204
180 DMWTC-----QKIPVEADFLYAYSTAPGYISWRNPKDGSWFIQSLCSML-KLYAHLKLEPMH 234
205 LITFVTRMA-----EALVQEGKARKTNPEIQSTLRKRLY 240
235 ILTRVNRKVATEPESPLDSTFPAKKQIPICIVSMLTKELY 274

RESULT 6
55315
y;Species: Homo sapiens (man)
y;Alternate names: cysteine proteinase CPP32
y;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
y;Accession: A55315; S58899; I39005
y;Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
y; Biol. Chem. 269, 30761-30764, 1994
y;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
y;Reference number: A55315; MUID:95074098; PMID:7983002
y;Accession: A55315
y;Status: Preliminary
y;Molecule type: mRNA
y;Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666
y;Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.; Xu, V.L.; Miller, D.K.
y; Nature 376, 37-43, 1995
y;Title: Identification and inhibition of the ICE/CEP-3 protease necessary for mammalian
y;Reference number: S58899; MUID:95319529; PMID:7596430
y;Accession: S58899
y;Molecule type: Protein
y;Residues: 29-46;176-189,'R',191-193 <NIC>
y;Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier,
y; Cell 81, 801-809, 1995
y;Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
y;Reference number: A56924; MUID:95292347; PMID:7774019
y;Accession: I39005
y;Status: Preliminary
y;Molecule type: mRNA
y;Residues: 1-189,'E',191-277 <RES>
y;Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569
y;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 22.0%; Score 272.5; DB 2; Length 277;
Best Local Similarity 31.9%; Pred. No. 6.5e-14;
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

2y 9 EEKVDMSGAALALILCVTK-----AREGSEEDLDALHMFQRLPFSTMKRDPDA 58
34 DNSYKMDYPENGLCIIINRNFKSTGTSRSGVDVDAANLRTFRLKYEVRNKNLTLR 93
59 EQFOEELEKFOQAIDSRDPVSCAFVYLMARHREGFLKSGDG--EMVKLENLFEALNNKN 116
94 EEIVELMRDVSKEHDKSSFPV---VLSHGSEGIIFGTNGPVDLKKITNPF---RGDR 147
117 QCALRAKPKVYIIQACRGEQDPG-ETVGGDEIVWVKDSQPQIPTYTDALHVVSTVEGY 175
148 CRSITGPKLFIQACRGTELDGCIETDSGVDDMAC-----HKIPVDVFLYAYSTAPGY 203
176 IAYRHQKQSCFIQTLVDVFTK--RKGHILELLETVTRMA-EAELVQ---EGKARKTNP 229
204 YSWNSKDGSWFIQSLCAMLQYADKLEFHWILTRVNRKVATEFESFSDATPHAKKQIP 263
230 EIQSTLRKRLY 240
264 CIVSMLTKELY 274

RESULT 7
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JC7123

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caspase-9 long chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: JC7123
R;Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A;Reference number: JC7123; MUID:20001956; PMID:10529400
A;Accession: JC7123
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942
```

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Query Match 21.3%; Score 264.5; DB 2; Length 454;
Best Local Similarity 30.6%; Pred. No. 4.9e-13;
Matches 76; Conservative 36; Mismatches 89; Indels 47; Gaps 7;

Qy 29 REGSEEDLDALHMFQRLPFSTMKRDPDAEQ-----FOBELEKFOQAIDSRDPVSCAFV 84
Db 218 RTGSNTDRDKLEHRFRLWLFPMVEVKNDLTAKQVVTALMEMAHRNHLALD-----CFVV 270
Qy 85 VLMAHGRE-----GFLKGEDGEMVKLENLFEALNNKNCOALRAKPKVYIIQACRGQR 137
Db 271 VILSHGCOASHLQPPGAVYGTGCSVIEKIVNIFNGSCPSLGGKPKLFIQACGGEQK 330
Qy 138 D-----PGETVGGDEIVWVK-----DSPQTIPTYTDALHVVSTVEGYI 176
Db 331 DHGFEVACTSSQGRITLSDSEDPATPFQEGPRPLDQDAVSSLPTPSDILVSYSTFGFV 390
Qy 177 AYRHQKQSCFIQTLVDVFTK--RKGHILELLETVTRMAEAEVQEGKARKTNPEIQST 234
Db 391 SWRDKSGSWYIETLGIILFQWARSEDLQSLLRV-----ANAVSEKGYKQIFGCENF 444
Qy 235 LRKRLYLQ 242
Db 445 LRKRLFFK 452
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RESULT 8

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A49429
interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Accession: A49429; T37312
C;Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A;Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int
A;Reference number: A49429; MUID:94061982; PMID:8242740
A;Accession: A49429
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-503 <YUA>
A;Cross-references: GB:L29052; NID:96503232; PIDN:AAA27982.2; PID:96503233
A;Note: sequence extracted from NCBI backbone (NCBI:139825, NCBI:139826)
A;Accession: T37312
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-417,'R',419-503 <YU2>
A;Cross-references: EMBL:L29052; PIDN:AAA27982.1
C;Genetics:
A;Gene: ced-3
A;Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3
```

Query Match

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Best Local Similarity 20.1%; Score 248.5; DB 2; Length 503;
Matches 68; Conservative 42; Mismatches 93; Indels 41; Gaps 6;

Qy 29 REGSEEDLDALHMFQRLPFSTMKRDPDAEQBELEKFOQAIDSRDPVSCAFVYLM 88
Db 259 RNGTKADKDLNLTFRCMGVTVICKNTLGRGMLLTIRDFAK----HESHGDSAILVILS 314
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89 HREGFLKGEDEGMVKLENFEALNNKNCQALRAKPKVYIIQACRGEQDPGETV-----143
315 HGEENVIIQVDDIPISHTHEIYDLNANAPRLANKPKIVFQACRGERDNGFPVLDSVD 374
144 -----GGDEIWMVKDSP-----QTIPTTALHVSIVVEGYIAYR 179
375 GVPAFLRRGWN-----RDGFLNFIQCVRPQVQVWRKKPQADILLIAYATAQYVSWR 429
180 HDQKSGCFIQLVDVFT--KRKGHILELLETVTRRMAEALVQEG-KARKTNPEIQSTLR 236
430 NSARGSWFIQACVCFVTHAKDMVDVVELLTVNKKVACGFTSGSNTILKOMPENTRELL 489
237 KRLY 240
490 KKFY 493

RESULT 9
67437
yestine proteinase (EC 3.4.22.-) P32 - rat (fragment)
;Species: Rattus norvegicus (Norway rat)
;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
;Accession: I67437
;Flaws: J.A.; Kugu, K.; Trbovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Til
ndocrinology 136, 5042-5053, 1995
;Title: Interleukin-1-beta-converting enzyme-related proteases (IRpe) and mammalian cel
ulosa cells of the ovarian follicle.
;Reference number: I53300; MUID:96042508; PMID:7588240
;Accession: I67437
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1-212 <RES>
;Cross-references: EMBL:U34688; NID:G1004370; PIDN:AAC52261.1; PID:G1004371
;Keywords: cysteine proteinase; hydrolase

Query Match 19.9%; Score 246.5; DB 2; Length 212;
Best Local Similarity 31.5%; Pred. No. 5e-12;
Matches 69; Conservative 34; Mismatches 89; Indels 27; Gaps 8;

y 9 BEKDMGSAALALILCVT-----KAREGSEDLDALEHMFQRLRFESTWKEDPTA 58
b 5 DSSVMDYVPEGLCIINNNFKHSGMGARNGTDVDAANLRETFWALKYEVNRKNDLTR 64
y 59 EQFOELEKFOQAIDSRDPSVCAFLVMAHGREGLKGEDGMVKLENFEALNNKNCQ 118
b 65 FEIMELMDSVSKEDHKSRSFVC---VILSHGDEGVIFGTNGP-VDLKKLTSFFRGDYCR 120
y 119 ALRAKPKVYIIQACRGEQDPG-ETVGG--DEIVMWIKDSPQTIPTTYTDALEHVSIVVEGY 175
b 121 SLTKPKLFIQACRGTSLSGIETSGADDDVAC-----QKKPEADFLIAYSSAPFY 174
y 176 IAYRHDKGSCFIQTLVDVFTVTKRKHILELLETVTRRMAEALVQEGKARKTNPEI 211
b 175 YSWNSRGGSWFIQSLC-AMKLKYAHKLEFPMHILTRVNR 212

RESULT 10
102635
CE-LAP6 - human
;Species: Homo sapiens (man)
;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
;Accession: G02635
;Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
submitted to the EMBL Data Library, April 1996
;Reference number: H01513
;Accession: G02635
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: mRNA
;Residues: 1-416 <DUA>
;Cross-references: EMBL:U56390; NID:G1336026; PIDN:AAC50640.1; PID:G1336027

Query Match 19.3%; Score 239.5; DB 2; Length 416;
Best Local Similarity 28.7%; Pred. No. 3.9e-11;

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Matches 72; Conservative 46; Mismatches 84; Indels 49; Gaps 9;
QY 27 KAREGSEDLDALEHMFQRLRFESTWKEDPTAEOFOELEKFOQAIDSRD--PVSCAFV 84
Db 178 RTRGSGNIDCKLARRRSSLHFVVEVKGDLTAKKMYLALLEL-----AQDHGALDCCVV 232
QY 85 VLMAGRE-----GFLKGEDGMVKLENFEALNNKNCQALRAKPKVYIIQACRGEQ 137
Db 233 VILSHGQASHLPQGVAYGTGCPVSEKIVNIFNGTSCPSLGGKPKLFFIQAACGGQK 292
QY 138 DPG-----ETVGG-----DEIVMWIKDSPQTIPTTYTDALEHVSIVVEGY 171
Db 293 DHGEVASTSPEDSPGSPNPDPATPFQEGRLRFDQL-----DAISSLTPTSDIFVSYST 347
QY 172 VEGYIAYRHDKGSCFIQTLVDVFTVTKRKHILELLETVTRRMAEALVQEGKARKTNPEI 231
Db 348 PFGFVSWRDPKSGSWYVETLDDIF-EGWAH-SSDQLSLRLRVANAVSK--GIYKOMPGC 403
QY 232 QSTLRKRLYLQ 242
Db 404 FNFELKKLFFK 414

RESULT 11
T20038
hypothetical protein C48D1.2 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
;Accession: T20038
;R.Burton, J.
submitted to the EMBL Data Library, October 1996
;Reference number: Z19214
;Accession: T20038
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-495 <WIL>
;Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
;Experimental source: clone C48D1
;Genetics:
;Gene: CESP:C48D1.2
;Map position: 4
;Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 18.6%; Score 230; DB 2; Length 495;
Best Local Similarity 27.6%; Pred. No. 2.6e-10;
Matches 60; Conservative 39; Mismatches 78; Indels 40; Gaps 5;

QY 29 REGSEDLDALEHMFQRLRFESTWKEDPTAEOFOELEKFOQAIDSRDPSVCAFLVMA 88
Db 258 RGTAKDKNLTLNFRGMGYTVICKNLGTGRGMLTIRDFAK-----HSHGDSATLVILS 313
QY 89 HREGFLKGEDEGMVKLENFEALNNKNCQALRAKPKVYIIQACRGEQDPGETV-----143
Db 314 HGEENVIIQVDDIPISHTHEIYDLNANAPRLANKPKIVFQACRGERDNGFPVLDSVD 373
QY 144 -----GGDEIWMVKDSP-----QTIPTTALHVSIVVEGYIAYR 179
Db 374 GVPAFLRRGWN-----RDGFLNFIQCVRPQVQVWRKKPQADILLIAYATAQYVSWR 428

RESULT 12
B56084
interleukin-1beta converting enzyme gamma isozyme - human
;Species: Homo sapiens (man)
;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
;Accession: B56084
;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
;Title: Cloning and expression of four novel isoforms of human interleukin-1beta convert

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;Reference number: A56084; MUID:95181414; PMID:7876192
;Accession: B56084
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-311 <ALN>
;Cross-references: GB:U13698; NID:G717041; PIDN:AAC50108.1; PID:G717042
;Genetics:
;Gene: IL1BCE
;Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 311;
Best Local Similarity 29.5%; Pred. NO. 3.1e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Y 15 SGAALAILCVTK-----AREGSEEDLDALHMFRLQRPSTMKRDPPTAEQFQEELEKQ 69
b 67 SRTLLALICNEEFSDIPRTGAEDVTGTMLLQNLGYSVDVKKNLTASDMTTELEAFA 126
Y 70 QAIDSRDPVSCAFVYLMAHG-REGFLKGEDGMV-----KLENLFEALNNKNCQALRAKP 124
b 127 HRPEHKTS--DSTFLVFMHSHGIREGICGKHSEQVPDILQLNAIFNMLNTKNCPSLKDKP 184
Y 125 KYVILIQACRGEQDPTGVTGDEIVMWIKDS-----POTIPTYTDAL---HV----- 168
b 185 KVIILIQACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEFEEDDAIKKAHIEKDF 234
Y 169 ---YSTVEGYIAYRHDKQSCFIOTLVDFVTKRKHILEL-----LTEVTRMAEAEVLQ 220
b 235 IAFCSSTPDNVSRRHPTMGVSFVIGRLIE-----HMQEYACSDVEEIFRKVRFSFEQP 287
Y 221 EGKARKTNPIQSTLRKRLYL 241
b 288 DGRAQMPTE-RVLTTRCFYL 307

RESULT 13
A56084
Interleukin-1 beta converting enzyme beta isozyme - human
C:Species: Homo sapiens (man)
J:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
J:Accession: A56084
J:Alnemrl, E.S.; Fernandes-Alnemrl, T.; Litwack, G.
J: Biol. Chem. 270, 4312-4317, 1995
A:Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver
A:Reference number: A56084; MUID:95181414; PMID:7876192
A:Accession: A56084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-383 <ALN>
A:Cross-references: GB:U13697; NID:G717039; PIDN:AAC50107.1; PID:G717040
C:Genetics:
A:Gene: IL1BCE
C:Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 383;
Best Local Similarity 29.5%; Pred. NO. 3.9e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Y 15 SGAALAILCVTK-----AREGSEEDLDALHMFRLQRPSTMKRDPPTAEQFQEELEKQ 69
b 139 SRTLLALICNEEFSDIPRTGAEDVTGTMLLQNLGYSVDVKKNLTASDMTTELEAFA 198
Y 70 QAIDSRDPVSCAFVYLMAHG-REGFLKGEDGMV-----KLENLFEALNNKNCQALRAKP 124
b 199 HRPEHKTS--DSTFLVFMHSHGIREGICGKHSEQVPDILQLNAIFNMLNTKNCPSLKDKP 256
Y 125 KYVILIQACRGEQDPTGVTGDEIVMWIKDS-----POTIPTYTDAL---HV----- 168
b 257 KVIILIQACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEFEEDDAIKKAHIEKDF 306
Y 169 ---YSTVEGYIAYRHDKQSCFIOTLVDFVTKRKHILEL-----LTEVTRMAEAEVLQ 220
b 307 IAFCSSTPDNVSRRHPTMGVSFVIGRLIE-----HMQEYACSDVEEIFRKVRFSFEQP 359

;Reference number: A56084; MUID:95181414; PMID:7876192
;Accession: B56084
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-311 <ALN>
;Cross-references: GB:U13698; NID:G717041; PIDN:AAC50108.1; PID:G717042
;Genetics:
;Gene: IL1BCE
;Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 311;
Best Local Similarity 29.5%; Pred. NO. 3.1e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Y 15 SGAALAILCVTK-----AREGSEEDLDALHMFRLQRPSTMKRDPPTAEQFQEELEKQ 69
b 67 SRTLLALICNEEFSDIPRTGAEDVTGTMLLQNLGYSVDVKKNLTASDMTTELEAFA 126
Y 70 QAIDSRDPVSCAFVYLMAHG-REGFLKGEDGMV-----KLENLFEALNNKNCQALRAKP 124
b 127 HRPEHKTS--DSTFLVFMHSHGIREGICGKHSEQVPDILQLNAIFNMLNTKNCPSLKDKP 184
Y 125 KYVILIQACRGEQDPTGVTGDEIVMWIKDS-----POTIPTYTDAL---HV----- 168
b 185 KVIILIQACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEFEEDDAIKKAHIEKDF 234
Y 169 ---YSTVEGYIAYRHDKQSCFIOTLVDFVTKRKHILEL-----LTEVTRMAEAEVLQ 220
b 235 IAFCSSTPDNVSRRHPTMGVSFVIGRLIE-----HMQEYACSDVEEIFRKVRFSFEQP 287
Y 221 EGKARKTNPIQSTLRKRLYL 241
b 288 DGRAQMPTE-RVLTTRCFYL 307

RESULT 14
A42677
Interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
C:Species: Homo sapiens (man)
J:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
J:Accession: A42677; S21734; S24164
J:Carrett, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
Genomics 20, 468-473, 1994
A:Title: Molecular characterization of the gene for human interleukin-1beta converting e
A:Reference number: A54263; MUID:94307734; PMID:8034320
A:Accession: A54263
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-404 <CE2>
A:Cross-references: GB:L27475
R:Carretti, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
Science 256, 97-100, 1992
A:Title: Molecular cloning of the interleukin-1beta converting enzyme.
A:Reference number: A42677; MUID:92229430; PMID:1373520
A:Accession: A42677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <CE2>
A:Cross-references: GB:M87507; NID:9435598; PIDN:AAA66942.1; PID:gl86286
R:Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.
J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Linjuco, G.; Palyha, O.C.; Raju, S.M.; Rol
Sci. M.J.
Nature 356, 768-774, 1992
A:Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proce
A:Reference number: S21734; MUID:92244338; PMID:1574116
A:Accession: S21734
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <THO>
A:Cross-references: EMBL:X55019; NID:G33792; PIDN:CAA46153.1; PID:G33793
R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.;
Arch. Biochem. Biophys. 296, 698-703, 1992
A:Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
A:Reference number: S24164; MUID:92337439; PMID:1321594
A:Accession: S24164
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>
C:Genetics:
A:Gene: GDB:IL1BC
A:Cross-references: GDB:132368; OMIM:147678
A:Map position: 11q23-11q23
C:Keywords: cysteine proteinase; hydrolase

Query Match 18.2%; Score 226; DB 2; Length 404;
Best Local Similarity 29.5%; Pred. NO. 4.2e-10;
Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

Y 15 SGAALAILCVTK-----AREGSEEDLDALHMFRLQRPSTMKRDPPTAEQFQEELEKQ 69
b 160 SRTLLALICNEEFSDIPRTGAEDVTGTMLLQNLGYSVDVKKNLTASDMTTELEAFA 219
Y 70 QAIDSRDPVSCAFVYLMAHG-REGFLKGEDGMV-----KLENLFEALNNKNCQALRAKP 124
b 220 HRPEHKTS--DSTFLVFMHSHGIREGICGKHSEQVPDILQLNAIFNMLNTKNCPSLKDKP 277
Y 125 KYVILIQACRGEQDPTGVTGDEIVMWIKDS-----POTIPTYTDAL---HV----- 168
b 278 KVIILIQACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEFEEDDAIKKAHIEKDF 327
Y 169 ---YSTVEGYIAYRHDKQSCFIOTLVDFVTKRKHILEL-----LTEVTRMAEAEVLQ 220
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[illegible]

Search completed: March 19, 2004, 11:24:53
Job time : 15.498 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 19, 2004, 11:24:16 ; Search time 34.2271 Seconds
(without alignments)
1830.924 Million cell updates/sec

Title: US-09-989-903-5

Perfect score: 1239

Sequence: 1 MSNPRSEEEKYDMSGAAAL.....KARKTNPEIQSTIRKELYLQ 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgm2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgm2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgm2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
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- 8: /cgm2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
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- 10: /cgm2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgm2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgm2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
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- 16: /cgm2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 17: /cgm2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 18: /cgm2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1239	100.0	242	9	US-09-989-903-5
2	1239	100.0	242	14	US-10-068-564-5
3	1234	99.6	242	9	US-09-845-028-2
4	1234	99.6	242	10	US-09-851-873-105
5	1234	99.6	242	15	US-10-114-432-3
6	1234	99.6	242	15	US-10-114-432-15
7	1234	99.6	242	15	US-10-114-432-17
8	1234	99.6	242	15	US-10-114-432-18
9	1234	99.6	242	15	US-10-114-432-26
10	1234	99.6	242	15	US-10-114-432-27
11	1234	99.6	242	15	US-10-114-432-28
12	1234	99.6	242	15	US-10-114-432-30
13	1234	99.6	242	15	US-10-114-432-31
14	1234	99.6	242	15	US-10-114-432-67
15	1234	99.6	242	15	US-10-114-432-69

Sequence 71, Appl
Sequence 73, Appl
Sequence 13, Appl
Sequence 23, Appl
Sequence 37, Appl
Sequence 11, Appl
Sequence 22, Appl
Sequence 36, Appl
Sequence 9, Appl
Sequence 21, Appl
Sequence 66, Appl
Sequence 72, Appl
Sequence 24, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 29, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 34, Appl
Sequence 7, Appl
Sequence 5, Appl
Sequence 19, Appl
Sequence 64, Appl
Sequence 68, Appl
Sequence 35, Appl
Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-989-903-5
; Sequence 5, Application US/0989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-903-5

Query Match 100.0%; Score 1239; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSNPRSEEEKYDMSGAAALILCVTKAREGSEEDLDALHEMFQRLRFESTMKRDPTAEQ	60
DB	1	MSNPRSEEEKYDMSGAAALILCVTKAREGSEEDLDALHEMFQRLRFESTMKRDPTAEQ	60
QY	61	FOELEKPFQQAIDREDPVSCAFVLMHAGREGFLKGEDGEMVKLENLFEALNNKCOAL	120
DB	61	FOELEKPFQQAIDREDPVSCAFVLMHAGREGFLKGEDGEMVKLENLFEALNNKCOAL	120
QY	121	RAPKPVYIIQACRGEDPGETVGDEIVMVVKDSPTIITYTDALHVVSTVSGYIAYRH	180
DB	121	RAPKPVYIIQACRGEDPGETVGDEIVMVVKDSPTIITYTDALHVVSTVSGYIAYRH	180
QY	181	DQKSGCFITLVDVFTKRGHILELLTEVTRMAEAEVQEGKARKTNPIQSTLRKRLY	240

181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
241 LQ 242
241 LQ 242

RESULT 2
S-10-068-564-5
Sequence 5, Application US/10068564
Publication No. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068,564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
S-10-068-564-5

Query Match 100.0%; Score 1239; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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b 1 MSNPRSLSEEEKYDMSGAAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
Y 61 FOBELEKFOAIDSRDPSVCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
b 61 FOBELEKFOAIDSRDPSVCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
Y 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTIDALHVVSTVEGYIAYRH 180
b 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTIDALHVVSTVEGYIAYRH 180
Y 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
b 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
Y 241 LQ 242
b 241 LQ 242

RESULT 3
S-09-845-028-2
Sequence 2, Application US/09845028
Patent No. US20020081705A1
GENERAL INFORMATION:
APPLICANT: Mankovich, John
TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
FILE REFERENCE: BSI-111
CURRENT APPLICATION NUMBER: US/09/845,028
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/199,962
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
S-09-845-028-2
Query Match 99.6%; Score 1234; DB 9; Length 242;

Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSNPRSLSEEEKYDMSGAAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
DB 1 MSNPRSLSEEEKYDMSGAAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
QY 61 FOBELEKFOAIDSRDPSVCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOBELEKFOAIDSRDPSVCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTIDALHVVSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTIDALHVVSTVEGYIAYRH 180
QY 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
DB 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 4
US-09-851-873-105
; Sequence 105, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-105

Query Match 99.6%; Score 1234; DB 10; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MSNPRSLSEEEKYDMSGAAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
QY 61 FOBELEKFOAIDSRDPSVCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOBELEKFOAIDSRDPSVCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTIDALHVVSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTIDALHVVSTVEGYIAYRH 180
QY 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
DB 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 5
US-10-114-432-3
; Sequence 3, Application US/10114432
; Publication No. US20040019915A1

RESULT 6

241 LQ 242

RESULT 8
S-10-114-432-18
Sequence 18, Application US/10114432
Publication No. US20040019915A1

GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobivits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

S-10-114-432-18

Query Match 99.6%; Score 1234; DB 15; Length 242;

Best Local Similarity 99.6%; Pred. No. 3.9e-113;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 MSNPRSEEEKYDMSGAAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
b 1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
Y 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKQAL 120
b 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKQAL 120
Y 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTDTALHVTSTVEGYIAYRH 180
b 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTDTALHVTSTVEGYIAYRH 180
Y 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQSGKARKTNPEIQSTLRKRLY 240
b 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQSGKARKTNPEIQSTLRKRLY 240
Y 241 LQ 242
b 241 LQ 242

RESULT 9

S-10-114-432-26

Sequence 26, Application US/10114432
Publication No. US20040019915A1

GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobivits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 26

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-114-432-26

Query Match 99.6%; Score 1234; DB 15; Length 242;

Best Local Similarity 99.6%; Pred. No. 3.9e-113;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSEEEKYDMSGAAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
DB 1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKQAL 120
DB 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKQAL 120
QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTDTALHVTSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTDTALHVTSTVEGYIAYRH 180
QY 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQSGKARKTNPEIQSTLRKRLY 240
DB 181 DQKSCFIQTLVDVFTKRGHILELLTEVTRMAEALVQSGKARKTNPEIQSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 10

US-10-114-432-27

Sequence 27, Application US/10114432
Publication No. US20040019915A1

GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Robert K.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobivits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

FILE REFERENCE: 51158-20066.00

CURRENT APPLICATION NUMBER: US/10/114,432

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 88

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27

LENGTH: 242

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-114-432-27

Query Match 99.6%; Score 1234; DB 15; Length 242;

Best Local Similarity 99.6%; Pred. No. 3.9e-113;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSEEEKYDMSGAAALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
DB 1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPTAEQ 60
QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKQAL 120
DB 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKQAL 120
QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTDTALHVTSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGEQDPGETVGGDEIVMWIKDSPQTIPTTDTALHVTSTVEGYIAYRH 180


```

61 FQEELEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
61 FQEELEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
181 DQKGSCTIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240
181 DQKGSCTIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240
241 LQ 242
241 LQ 242

```

```

RESULT 14
3-10-114-432-67
Sequence 67, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
3-10-114-432-67

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Query Match          99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y      1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRPESTWKRDPDTAEQ 60
b      1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRPESTWKRDPDTAEQ 60

y      61 FQEELEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
b      61 FQEELEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGMVKLENLFEALNNKNCQAL 120

y      121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
b      121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180

y      181 DQKGSCTIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240
b      181 DQKGSCTIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240

y      241 LQ 242
b      241 LQ 242

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RESULT 15
3-10-114-432-69
Sequence 69, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:

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```

; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-69

Query Match          99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 3.9e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY     1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRPESTWKRDPDTAEQ 60
DB     1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRPESTWKRDPDTAEQ 60

QY     61 FQEELEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGMVKLENLFEALNNKNCQAL 120
DB     61 FQEELEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGMVKLENLFEALNNKNCQAL 120

QY     121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180
DB     121 RAKPKVYIIQACRGEQDPGETVGGDEIVVMVKDSPTIPTYTDALHVVSTVEGYIAYRH 180

QY     181 DQKGSCTIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240
DB     181 DQKGSCTIQLVDVFTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240

QY     241 LQ 242
DB     241 LQ 242

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Job time : 34.2271 secs

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GenCore version 5.1.6
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M protein - protein search, using sw model

un on: March 19, 2004, 11:20:21 ; Search time 15.9084 Seconds
(without alignments)
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itle: US-09-989-903-5
effect score: 1239
equence: 1 MSNPRLEEEKYDMSGALA.....KARKTNPEIQSLKRLYLQ 242

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Gapop 10.0 , Gapext 0.5

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otal number of hits satisfying chosen parameters: 389414

linimum DB seq length: 0
laximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/5A COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/5B COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1239	100.0	242	4	US-09-187-789-5
2	1065	86.0	214	4	US-09-187-789-9
3	934.5	75.4	260	4	US-09-187-789-2
4	934.5	75.4	260	4	US-09-139-600-2
5	890	71.8	230	4	US-09-187-789-7
6	293	23.6	74	4	US-09-187-789-63
7	293	23.6	74	4	US-09-139-600-58
8	289	23.3	421	4	US-08-983-502-10
9	289	23.3	421	4	US-09-516-747-10
10	289	23.3	421	5	PCT-US96-10521-10
11	289	23.3	435	3	US-08-258-287B-53
12	289	23.3	435	3	US-08-368-704C-51
13	289	23.3	435	4	US-09-561-756-9
14	289	23.3	435	4	US-09-227-721-9
15	289	23.3	435	4	US-08-816-075-2
16	289	23.3	435	4	US-08-724-378D-9
17	289	23.3	435	5	US-09-954-697-9
18	289	23.3	435	5	PCT-US94-07127A-4
19	289	23.3	441	3	US-08-258-287B-44
20	289	23.3	441	3	US-08-368-704C-43
21	279	22.5	435	4	US-08-231-289-10
22	278.5	22.5	277	2	US-08-890-542A-2
23	273.5	22.1	277	3	US-08-591-605-2
24	273.5	22.1	277	3	US-08-964-308-6
25	273.5	22.1	277	3	US-08-462-969B-4
26	273.5	22.1	277	3	US-08-964-313-6
27	273.5	22.1	277	4	US-09-089-138-6

28	273.5	22.1	277	4	US-09-124-934A-4	Sequence 4, Appli
29	273.5	22.1	277	4	US-08-334-251D-4	Sequence 4, Appli
30	272.5	22.0	277	4	US-09-561-756-12	Sequence 12, Appli
31	272.5	22.0	277	4	US-09-227-721-12	Sequence 12, Appli
32	272.5	22.0	277	4	US-08-983-502-30	Sequence 30, Appli
33	272.5	22.0	277	4	US-08-724-378D-5	Sequence 5, Appli
34	272.5	22.0	277	4	US-09-516-747-30	Sequence 30, Appli
35	272.5	22.0	277	4	US-09-954-697-12	Sequence 12, Appli
36	272.5	22.0	277	5	PCT-US96-10521-30	Sequence 30, Appli
37	270.5	21.8	277	4	US-09-291-289-11	Sequence 11, Appli
38	263.5	21.3	277	3	US-08-964-308-10	Sequence 10, Appli
39	263.5	21.3	277	3	US-08-964-313-10	Sequence 10, Appli
40	263.5	21.3	277	4	US-09-089-138-10	Sequence 10, Appli
41	257	20.7	503	3	US-08-258-287B-36	Sequence 36, Appli
42	257	20.7	503	3	US-08-368-704C-36	Sequence 36, Appli
43	256	20.7	303	4	US-09-561-756-24	Sequence 24, Appli
44	256	20.7	303	4	US-09-227-721-24	Sequence 24, Appli
45	256	20.7	303	4	US-08-556-627A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-5

Query Match	100.0%	Score	1239	DB	4	Length	242
Best Local Similarity	100.0%	Pred. No.	3.2e-122				
Matches	242	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MSNPRLEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPTEAQ	60				
Db	1	MSNPRLEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPTEAQ	60				
Qy	61	FOEELKFOQAIDSRDPPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKCOAL	120				
Db	61	FOEELKFOQAIDSRDPPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKCOAL	120				
Qy	121	RAPKVTYIQAACRGORDEGTGGDEIVMWKDSFOPIPTVDALHYSTVEGVIAVRH	180				
Db	121	RAPKVTYIQAACRGORDEGTGGDEIVMWKDSFOPIPTVDALHYSTVEGVIAVRH	180				
Qy	181	DQKSGCFIQLVDVFTKRGHILELLTEVTRMAELVQEGKARKTNPEIQSLTKELY	240				
Db	181	DQKSGCFIQLVDVFTKRGHILELLTEVTRMAELVQEGKARKTNPEIQSLTKELY	240				
Qy	241	LQ 242					
Db	241	LQ 242					

RESULT 2

US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
S-09-187-789-9

Query Match 86.0%; Score 934.5; DB 4; Length 214;
Best Local Similarity 88.0%; Pred. No. 5.3e-104;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
Y 1 MSNPRSLSEBKDYMSGAALALILCVTKAREGSEEDLDALHMFRLRPFSTMKRDPDPAEQ 60
b 1 MSNPRSLSEBKDYMSGAALALILCVTKAREGSEE-----34
Y 61 FQELEKFOAIDSRDPSVCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
b 35 --BELEKFOAIDSRDPSVCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 92
Y 121 RAKPKVYIIQACRGEQDPSVCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 180
b 93 RAKPKVYIIQACRGEQDPSVCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 152
Y 181 DQKSCFQIOTLVDFVTKRGHILELLTEVTRMAEAEIVQSGKARKTNPEIQSTLRKRLY 240
b 153 DQKSCFQIOTLVDFVTKRGHILELLTEVTRMAEAEIVQSGKARKTNPEIQSTLRKRLY 212
Y 241 LQ 242
b 213 LQ 214

RESULT 3
S-09-187-789-2
Sequence 2, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
S-09-187-789-2

Query Match 75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 3.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
Y 1 MSNPRSLSEBKDYMSGAALALILCVTKAREGSEEDLDALHMFRLRPFSTMKRDPDPAEQ 60
b 8 MSDPQPLQEBRYDMSGARLALTLCVTKAREGSEVDMEALRMFRYLKFESTMKRDPTAQ 67
Y 61 FQELEKFOAIDSRDPSVCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
b 68 FLEELDFQOTIDNWEPEVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 127
Y 121 RAKPKVYIIQACRGEQDPSVCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 180

Db 128 RGKPKVYIIQACRGEHDPGEELRGNELGGDEBELGGDE-VAVLKNPQSIPTTYDTLHI 186
QY 169 YSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELLTEVTRMAEAEIVQSGKARKTN 228
Db 187 YSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELLTEVTRMAEAEIVQSGKARKTN 246
QY 229 PEIQSTLRKRLY 242
Db 247 PEVQSTLRKRLY 260

RESULT 4
US-09-139-600-2
Sequence 2, Application US/09139600
Patent No. 6432628
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
US-09-139-600-2

Query Match 75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 3.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
QY 1 MSNPRSLSEBKDYMSGAALALILCVTKAREGSEEDLDALHMFRLRPFSTMKRDPDPAEQ 60
Db 8 MSDPQPLQEBRYDMSGARLALTLCVTKAREGSEVDMEALRMFRYLKFESTMKRDPTAQ 67
QY 61 FQELEKFOAIDSRDPSVCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 120
Db 68 FLEELDFQOTIDNWEPEVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 127
QY 121 RAKPKVYIIQACRGEQDPSVCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKCOAL 168
Db 128 RGKPKVYIIQACRGEHDPGEELRGNELGGDEBELGGDE-VAVLKNPQSIPTTYDTLHI 186
QY 169 YSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELLTEVTRMAEAEIVQSGKARKTN 228
Db 187 YSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELLTEVTRMAEAEIVQSGKARKTN 246
QY 229 PEIQSTLRKRLY 242
Db 247 PEVQSTLRKRLY 260

RESULT 5
US-09-187-789-7
Sequence 7, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 230

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Query Match      23.6%; Score 293; DB 4; Length 74;
Best Local Similarity 77.8%; Pred. No. 1.6e-23;
Matches 56; Conservative 8; Mismatches 0; Gaps 0;

QY      28 AREGSEEDLDALEHMFQLFESTMKRDPDTSQFOBELEKFKQAIDSRDEDPVSCAFVVLM 87
DB      1 AREGSEVDMEALRMFYLFKFEFTMKRDPDTSQOFLLELDDEFQOTIDNWEFPVSCAFVVLM 60

QY      88 AHGREGPLKGED 99
DB      61 AHGBEGLLKGED 72

RESULT 8
US-08-983-502-10
; Sequence 10, Application US/08983502
; Patent No. 6399327
; GENERAL INFORMATION:
; APPLICANT: David WALLACH
; APPLICANT: Mark P. BOLDIN
; APPLICANT: Tanya M. GONCHAROV
; APPLICANT: Yuri V. GOLTSEV
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; TITLE OF INVENTION: AND OTHER PROTEINS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,502
; FILING DATE: 16-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10521
; FILING DATE: 14-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,615
; FILING DATE: 16-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,986
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 115,319
; FILING DATE: 14-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 116,588
; FILING DATE: 27-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 117,932
; FILING DATE: 16-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-19
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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3-08-983-502-10

Query Match 23.3%; Score 289; DB 4; Length 421;
Best Local Similarity 31.1%; Pred. No. 5.2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
US-09-516-747-10

29 REGSEEDLDALEHMFQRLPSTMKRDPDTAQPQOELEKFOQAIDSREDPVSCAFVFLMA 88
188 RSGGDVHSTLVTFLKLGVDVHVLCDQTAQEMQKLNFAQ-LPAHRVTDSC-IVALLS 245
89 HGRGFLKGDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQORDPG- 140
246 HGVEGAIYGVGDKLLQLEVFQFLDNANCPSLQNKPMFFIACRGEDETDRGVDDQDGKN 305
141 -----ETVGGDIWVVIKDSPTIPTYTDALHVSIVTEGYIAYRHQKSGCFQTLLV 192
306 HAGSPGCEESDAGKE-----KLPMRLPTRSDMICGYACLGKGTAAAMNTRKSGSWYIEALA 360
193 DVFTKR--KGHILELLTEVTRMAEAEIVQSGKARKTN-----PEIQSTLRKRLYL 241
361 QVFSERACDMHVDMLVKVNALIKD-----REGYAPGTEFHRCKEMSEYCSITLCRHLYL 414

RESULT 9

S-09-516-747-10
Sequence 10, Application US/09516747
Patent No. 6586571

GENERAL INFORMATION:

APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya M. GONCHAROV
Yury V. GOLTSEV

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,747
FILING DATE: 01-Mar-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/983,502
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Broadway, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-516-747-10

Query Match 23.3%; Score 289; DB 4; Length 421;
Best Local Similarity 31.1%; Pred. No. 5.2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
US-09-516-747-10

QY 29 REGSEEDLDALEHMFQRLPSTMKRDPDTAQPQOELEKFOQAIDSREDPVSCAFVFLMA 88
DB 188 RSGGDVHSTLVTFLKLGVDVHVLCDQTAQEMQKLNFAQ-LPAHRVTDSC-IVALLS 245
QY 89 HGRGFLKGDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQORDPG- 140
DB 246 HGVEGAIYGVGDKLLQLEVFQFLDNANCPSLQNKPMFFIACRGEDETDRGVDDQDGKN 305
QY 141 -----ETVGGDIWVVIKDSPTIPTYTDALHVSIVTEGYIAYRHQKSGCFQTLLV 192
DB 306 HAGSPGCEESDAGKE-----KLPMRLPTRSDMICGYACLGKGTAAAMNTRKSGSWYIEALA 360
QY 193 DVFTKR--KGHILELLTEVTRMAEAEIVQSGKARKTN-----PEIQSTLRKRLYL 241
DB 361 QVFSERACDMHVDMLVKVNALIKD-----REGYAPGTEFHRCKEMSEYCSITLCRHLYL 414

RESULT 10

PCT-US96-10521-10
Sequence 10, Application PC/TUS9610521
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS

NUMBER OF SEQUENCES: 34

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10521-10

Query Match 23.3%; Score 289; DB 5; Length 421;
Best Local Similarity 31.1%; Pred. No. 5.2e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
US-09-516-747-10

Y 29 REGSEEDLDALHEMFQRLPFESTMKRDPTAEQFOBELEKFOQAIIDSRDPVSCAFVILMA 88
b 188 RSGGDVDHSTLVTFLKLLGYDVHVLCDQTAQEMQEKQLQNFQA-LPAHRVTDSC-IVALLS 245
Y 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQORDPG-----140
b 246 HGVEGAIYGVGKLLQLQEVFQLFNANCPSLQNKPKMFFIACRGGDETDGVDGQDQGN 305
Y 141 -----ETVGGDEIWMVKIDSPQTIPTYTDALHVTSTVEGYIAYRHDKGSCFIOTLV 192
b 306 HAGSPGCEESDAGKE-----KLPKMRLPTRSDMICGYACLKGTAAAMRNTKRGSWYIEALA 360
Y 193 DVFTKR--KGHILELLTEVTRMAEAEVQEGKAKTN-----PEIQSTLRKRLYL 241
b 361 QVFSERACDMHVDMLVKVNALIKD-----REGYAPGTGFHRCKEMSEYCVSTLCRHLYL 414

RESULT 11
US-08-258-287B-53
Sequence 53, Application US/08258287B
Patent No. 6083735
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,287B
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3920001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-258-287B-53

Query Match 23.3%; Score 289; DB 3; Length 435;
Best Local Similarity 31.1%; Pred. No. 5.4e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
Y 29 REGSEEDLDALHEMFQRLPFESTMKRDPTAEQFOBELEKFOQAIIDSRDPVSCAFVILMA 88
b 202 RSGGDVDHSTLVTFLKLLGYDVHVLCDQTAQEMQEKQLQNFQA-LPAHRVTDSC-IVALLS 259
Y 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQORDPG-----140
b 260 HGVEGAIYGVGKLLQLQEVFQLFNANCPSLQNKPKMFFIACRGGDETDGVDGQDQGN 319

QY 141 -----ETVGGDEIWMVKIDSPQTIPTYTDALHVTSTVEGYIAYRHDKGSCFIOTLV 192
DB 320 HAGSPGCEESDAGKE-----KLPKMRLPTRSDMICGYACLKGTAAAMRNTKRGSWYIEALA 374
QY 193 DVFTKR--KGHILELLTEVTRMAEAEVQEGKAKTN-----PEIQSTLRKRLYL 241
DB 375 QVFSERACDMHVDMLVKVNALIKD-----REGYAPGTGFHRCKEMSEYCVSTLCRHLYL 428

RESULT 12
US-08-368-704C-51
Sequence 51, Application US/08368704C
Patent No. 6087160
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,704C
FILING DATE: 4-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3920002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-368-704C-51

Query Match 23.3%; Score 289; DB 3; Length 435;
Best Local Similarity 31.1%; Pred. No. 5.4e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
QY 29 REGSEEDLDALHEMFQRLPFESTMKRDPTAEQFOBELEKFOQAIIDSRDPVSCAFVILMA 88
DB 202 RSGGDVDHSTLVTFLKLLGYDVHVLCDQTAQEMQEKQLQNFQA-LPAHRVTDSC-IVALLS 259
QY 89 HGREGLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQORDPG-----140
DB 260 HGVEGAIYGVGKLLQLQEVFQLFNANCPSLQNKPKMFFIACRGGDETDGVDGQDQGN 319
QY 141 -----ETVGGDEIWMVKIDSPQTIPTYTDALHVTSTVEGYIAYRHDKGSCFIOTLV 192
DB 320 HAGSPGCEESDAGKE-----KLPKMRLPTRSDMICGYACLKGTAAAMRNTKRGSWYIEALA 374

y 193 DVFTKR--KGHILELLETVTRRABAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
b 375 QVESBRACDMHVADMLVKYNALIKD----REGYAPGTEBFHRCCKEMSEYCYSTLCRHLYL 428

earch completed: March 19, 2004, 11:25:37
ob time : 16.9084 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1234	99.6	242	3	AA973214	Amino aci
2	1234	99.6	242	5	AA977980	Full+ leng
3	1189	96.0	242	5	AA977984	Full+ leng
4	1186	94.1	229	3	AA976885	Amino aci
5	1065	86.0	214	3	AA973216	Amino aci
6	934.5	75.4	257	3	AA976886	Amino aci
7	934.5	75.4	281	2	AA973592	Mouse cas
8	934.5	75.4	281	3	AA973213	Amino aci
9	890	71.8	230	3	AA973215	Amino aci
10	472.5	38.1	234	5	AA972982	Human asp
11	472.5	38.1	398	5	AB976499	DNA encod
12	295	23.8	42	5	AB910110	Mouse cas
13	293	23.6	452	7	AD579812	Rat caspa
14	293	23.6	452	7	AD563000	Rat Prote
15	289	23.3	435	2	AA966771	Human int
16	289	23.3	435	2	AA98462	Human Ice
17	289	23.3	435	2	AA90703	Interleuk
18	289	23.3	435	2	AA926274	Cell deat
19	289	23.3	435	2	AA921716	Amino aci
20	289	23.3	435	3	AB14257	Human Ich
21	289	23.3	435	4	AAE00599	Human cas
22	289	23.3	435	5	AB701217	Amino aci
23	289	23.3	435	5	ABJ01217	Human cas
24	289	23.3	435	7	AD633002	Human Pro
25	289	23.3	441	2	AA967668	Human int

CC The present sequence represents a human caspase-14 polypeptide. The
CC polypeptide is a cell death specific protease, and is an apoptosis
CC stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-
CC -14 antibodies are useful for treating or reducing the severity of
CC pathological conditions associated with increased or decreased levels of

C apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
 C diseases and ischemic injury are treated by administering anti-caspase-14
 C antibodies. The antibody is useful for determining the presence or the
 C level of caspase-14 in tissue sample and also for the isolation of
 C caspase-14 with apoptotic activity or in screening assay to identify an
 C agent that inhibits heterodimer or heterotetramer formation and
 C therefore, apoptosis
 X
 Q Sequence 242 AA;

Query Match 99.6%; Score 1234; DB 3; Length 242;
 Best Local Similarity 99.6%; Pred. No. 1.5e-120;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 MSNPRSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPDPAEQ 60
 b 1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPDPAEQ 60

Y 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQOAL 120
 b 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQOAL 120

Y 121 RAKPKVYIIQACRGEQDPGETVGGDEIWMVVKDPSQTIPTTYTDALHVIYSTVEGYIAYRH 180
 b 121 RAKPKVYIIQACRGEQDPGETVGGDEIWMVVKDPSQTIPTTYTDALHVIYSTVEGYIAYRH 180

Y 181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240
 b 181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240

Y 241 LQ 242
 b 241 LQ 242

RESULT 2
 AG77980
 D AAG77980 standard; protein; 242 AA.
 X
 C AAG77980;
 X
 T 05-APR-2002 (first entry)
 X
 E Full-length human caspase-14.
 X
 W Human; caspase-14; anti-apoptotic; apoptosis.
 X
 S Homo sapiens.
 X
 N WO200181595-A2.
 X
 D 01-NOV-2001.
 X
 F 27-APR-2001; 2001WO-US013831.
 X
 R 27-APR-2000; 2000US-0199962P.
 X
 A (KNOL) KNOLL GMBH.
 X
 I Mankovich JA;
 X
 R WPI; 2002-041410/05.
 R N-PSDB; AAK98248.
 X
 T Novel isolated human caspase-14 proteins and nucleic acid sequences,
 T useful for identifying modulators of caspase-14 protein that are useful
 T for modulating apoptosis.
 X
 S Claim 20; Fig 1; 58pp; English.
 X
 X The sequence represents the novel full-length human caspase-14 protein,
 C referred to as "Caspase-14 NRW" in the specification. The invention
 C relates to a novel isolated human caspase-14 protein comprising an amino

CC acid sequence with MSNPRSEEE, at its amino terminus. The caspase-14 of
 CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
 CC of caspase-14 activity. The polypeptide is useful for identifying a
 CC compound which is a modulator of human caspase-14 activity, and is also
 CC useful for identifying a compound which modulates the interaction of
 CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
 CC for isolating the protein by standard techniques, and for detecting
 CC caspase-14 to evaluate the abundance and expression pattern. The antibody
 CC is also useful for diagnostically monitoring protein levels in a tissue
 CC as a part of a clinical testing procedure. The polypeptide is useful as a
 CC protease to cleave substrates and for inducing apoptosis in cells, in
 CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
 CC assay to identify other proteins that interact with human caspase-14
 CC protein
 XX
 SQ Sequence 242 AA;

Query Match 99.6%; Score 1234; DB 5; Length 242;
 Best Local Similarity 99.6%; Pred. No. 1.5e-120;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPDPAEQ 60
 Db 1 MSNPRSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPDPAEQ 60

QY 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQOAL 120
 Db 61 FQEELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKQOAL 120

QY 121 RAKPKVYIIQACRGEQDPGETVGGDEIWMVVKDPSQTIPTTYTDALHVIYSTVEGYIAYRH 180
 Db 121 RAKPKVYIIQACRGEQDPGETVGGDEIWMVVKDPSQTIPTTYTDALHVIYSTVEGYIAYRH 180

QY 181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240
 Db 181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEALVQEGKARKTNPEIQSTLRKRLY 240

QY 241 LQ 242
 Db 241 LQ 242

RESULT 3
 AAG77984
 ID AAG77984 standard; protein; 242 AA.
 XX
 AC AAG77984;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE Full-length human caspase-14 old.
 XX
 KW Human; caspase-14; anti-apoptotic; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200181595-A2.
 XX
 PD 01-NOV-2001.
 XX
 X 27-APR-2001; 2001WO-US013831.
 XX
 PR 27-APR-2000; 2000US-0199962P.
 XX
 X (KNOL) KNOLL GMBH.
 PA
 X Mankovich JA;
 XX
 X WPI; 2002-041410/05.
 XX
 X Novel isolated human caspase-14 proteins and nucleic acid sequences,
 PT useful for identifying modulators of caspase-14 protein that are useful
 PT for modulating apoptosis.

Example; Fig 1; 58pp; English.

The sequence represents the full-length human caspase-14 protein, referred to as "Caspase-14 Old" in the specification. The invention relates to a novel isolated human caspase-14 protein comprising an amino acid sequence with MSNPSLEE, at its amino terminus. The caspase-14 of the invention has anti-apoptotic activity. Caspase-14 acts as a modulator of caspase-14 activity. The polypeptide is useful for identifying a compound which is a modulator of human caspase-14 activity, and is also useful for identifying a compound which modulates the interaction of caspase-14 with a target molecule. An antibody to caspase-14 is useful for isolating the protein by standard techniques, and for detecting caspase-14 to evaluate the abundance and expression pattern. The antibody is also useful for diagnostically monitoring protein levels in a tissue or sample. The polypeptide is useful as a tissue or sample for screening assays, and as a bait protein in a two-hybrid or three-hybrid assay to identify other proteins that interact with human caspase-14 protein.

Sequence 242 AA;

Query Match 96.0%; Score 1189; DB 5; Length 242;
Best Local Similarity 99.6%; Pred. No. 7.6e-116;
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
10 EKYDMSGALALILCVTKAREGSEEDLDALHMPQRLRFSTMKRDPDTAQFOBELEKFO 69
10 EKYDMSGALALILCVTKAREGSEEDLDALHMPQRLRFSTMKRDPDTAQFOBELEKFO 69
70 QAIDREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKCOALRAKPKVYII 129
70 QAIDREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKCOALRAKPKVYII 129
130 QACRGEORDPGTGSGDEIVMWIKDSPOTIPTYTDLHVSTVEGYIAYRHDKGSCFIQ 189
130 QACRGEORDPGTGSGDEIVMWIKDSPOTIPTYTDLHVSTVEGYIAYRHDKGSCFIQ 189
190 TLVDVFTKKGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLYLQ 242
190 TLVDVFTKKGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLYLQ 242

RESULT 4
AY68865
RAY68865 standard; protein; 229 AA.

AY68865;
15-MAY-2000 (first entry)
Amino acid sequence of a human caspase-like polypeptide.
Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
keratinisation; wound healing.
Homo sapiens.
WO200004169-A1.
27-JAN-2000.
12-JUL-1999; 99WO-EP004939.
17-JUL-1998; 98EP-0020422.
(VLAAS) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
WPI; 2000-182433/16.
N-PSDB; AAZ60684.

XX New murine and human caspase homologues useful for treating skin related disorders.

Claim 2; Page 53-54; 68pp; English.

The present sequence represents a human caspase-like polypeptide. The specification also describes a murine caspase-like polypeptide. Caspases are cysteinyl aspartate-specific proteinases which play a central role in apoptosis. The polypeptides of the invention are related to human and murine caspase-2 and human caspase-9, and possess all of the typical amino acids involved in catalysis, including the QACRG box, and contain no or only a very short prodomain. mRNA expression of the homologues of the invention is predominant in the skin. The caspase-like polypeptides are useful for treating human or animal diseases, such as skin diseases. They are also useful for screening for compounds that modulate its activity, i.e. agonists, antagonists, and inhibitors. The caspase-like polypeptides and polynucleotides are useful for modulating keratinisation, for diagnosing and treating inappropriate wound healing

Sequence 229 AA;

Query Match 94.1%; Score 1166; DB 3; Length 229;
Best Local Similarity 99.6%; Pred. No. 1.8e-113;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
14 MSGAALALILCVTKAREGSEEDLDALHMPQRLRFSTMKRDPDTAQFOBELEKFOAID 73
1 MSGAALALILCVTKAREGSEEDLDALHMPQRLRFSTMKRDPDTAQFOBELEKFOAID 60
74 SREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKCOALRAKPKVYIIQACR 133
61 SREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKCOALRAKPKVYIIQACR 120
134 GEORDPGTGSGDEIVMWIKDSPOTIPTYTDLHVSTVEGYIAYRHDKGSCFIQTLVD 193
121 GEORDPGTGSGDEIVMWIKDSPOTIPTYTDLHVSTVEGYIAYRHDKGSCFIQTLVD 180
194 VFTKKGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLYLQ 242
181 VFTKKGHILELLTEVTRMAEAEVLQEGKARKTNPEIQSTLRKRLYLQ 229

RESULT 5
AY93216
ID AAY93216 standard; protein; 214 AA.
AY93216;
04-SEP-2000 (first entry)
Amino acid sequence of a human caspase-14 splice variant.
Caspase-14; cell death specific protease; apoptosis stimulator;
apoptosis; AIDS; neurodegenerative disease; ischemic injury.
Homo sapiens.
Key Location/Qualifiers
Active-site 102..106
WO200028047-A1.
18-MAY-2000.
29-OCT-1999; 99WO-US025523.
06-NOV-1998; 98US-00187789.
(UYJE-) UNIV JEFFERSON THOMAS.
Alnemri ES, Fernandez-Alnemri T;
XX

WPI; 2000-375558/32.
N-PSDB; AAA15166.
Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
Claim 42; Fig 9; 78pp; English.
The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence of the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis
Sequence 214 AA;
Query Match 86.0%; Score 1065; DB 3; Length 214;
Best Local Similarity 88.0%; Pred. No. 6.2e-103;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
1 MSNPSLEEKYDMSGALALILCVTKAREGSEBDLDALEHMFQRLRFESTMKRDPTAEQ 60
1 MSNPSLEEKYDMSGALALILCVTKAREGSEB-----
61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
35 --EELEKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 92
121 RAKPKVYIIQACRGQRDPGETVGGDEIVMWIKDSPQITPTDTHLVSTVSGYIAYRH 180
93 RAKPKVYIIQACRGQRDPGETVGGDEIVMWIKDSPQITPTDTHLVSTVSGYIAYRH 152
181 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEAEVLQVGKARKTNPEIQSTLRKRLY 240
153 DQKSGCFIOTLVDFVTKRGHILELLTEVTRMAEAEVLQVGKARKTNPEIQSTLRKRLY 212
241 LQ 242
213 LQ 214
RESULT 6
AY68864
D AAY68864 standard; protein; 257 AA.
K AAY68864;
I 16-MAY-2000 (first entry)
K Amino acid sequence of a murine caspase-like polypeptide.
K Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
K keratinisation; wound healing.
S Mus musculus.
N WO200004169-A1.
D 27-JAN-2000.
X 12-JUL-1999; 99WO-BF004939.
F 17-JUL-1998; 98EP-00202422.
R (VLA--) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
A

PI Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
XX WPI; 2000-182433/16.
DR N-PSDB; AAZ60683.
XX New murine and human caspase homologues useful for treating skin related disorders.
PT
PT
XX Claim 1; Page 51-52; 68pp; English.
XX The present sequence represents a murine caspase-like polypeptide. The specification also describes a human caspase-like polypeptide. Caspases are cysteinyl aspartate-specific proteinases which play a central role in apoptosis. The polypeptides of the invention are related to human and murine caspase-2 and human caspase-9, and possess all of the typical amino acids involved in catalysis, including the QACRG box, and contain no or only a very short prodomain. mRNA expression of the homologues of the invention is predominant in the skin. The caspase-like polypeptides are useful for treating human or animal diseases, such as skin diseases. They are also useful for screening for compounds that modulate its activity, i.e. agonists, antagonists, and inhibitors. The caspase-like polypeptides and polynucleotides are useful for modulating keratinisation, for diagnosing and treating inappropriate wound healing
Sequence 257 AA;
Query Match 75.4%; Score 934.5; DB 3; Length 257;
Best Local Similarity 70.9%; Pred. No. 3.8e-89;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
QY 1 MSNPSLEEKYDMSGALALILCVTKAREGSEBDLDALEHMFQRLRFESTMKRDPTAEQ 60
DB 5 MSDFPQLEERYDMSGARLALTLCVTKAREGSEVDMEALRMFRLKFESTMKRDPTAQ 64
QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 65 FLEELDFQOTIDNWEFVSCAFVVLMAHGEGLKGEDGEMVKLENLFEALNNKNCQAL 124
QY 121 RAKPKVYIIQACRGQRDPG-----ETVGGDEIVMWIKDSPQITPTDTHLV 168
DB 125 RGPVKVYIIQACRGQRDPGSELNGEELGGDEELGGDE--VALKNNPQSIPTDTHL 183
QY 169 YSTVEGYIAYRHDKGSCFIOTLVDFVTKRGHILELLTEVTRMAEAEVLQVGKARKTN 228
DB 184 YSTVEGYIAYRHDKGSGFIOTLVDFVTKRGHILELLTEVTRMAEAEVLQVGKARKTN 243
QY 229 PEIQTSLRKRLYLQ 242
DB 244 PEVQSTLRKRLYLQ 257
RESULT 7
AAW93592
ID AAW93592 standard; protein; 281 AA.
XX AAW93592;
AC AAW93592;
DT 21-JUN-1999 (first entry)
XX Mouse caspase-14 protein.
DE
XX Caspase-14; murine; protease; treatment; apoptotic-related disease;
KW autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
KW neurodegenerative disease; ischaemic injury; anti-idiotypic antibody;
KW caspase-14 processing activity; epitope; competitor; modulator.
XX Mus sp.
OS
XX WO9910504-A2.
FN
XX 04-MAR-1999.
PD
XX 26-AUG-1998; 98WO-US017715.
PF

X R 26-AUG-1997; 97US-0056986P.
X A (IDUN-) IDUN PHARM INC.
X I Alnemri ES, Fernandes-Alnemri T;
X R WPI; 1999-204670/17.
X R N-PSDB; AAX23515.
X T Newly isolated polynucleotide encoding a caspase-14 polypeptide - useful
T for identifying (ant)agonists that are useful in the diagnosis and
T treatment of apoptosis-related diseases.
X X Claim 4; Fig 1; 59pp; English.
X C This invention describes a novel murine caspase-14 which has protease
C activity. The caspase-14 polypeptide is useful for identifying
C (ant)agonists of the polypeptide, where enzyme activity is measured with
C a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated
C caspase-14 is useful for identifying inhibitors or enhancers of caspase-
C 14 activity. The compounds identified by both methods form pharmaceutical
C compositions for treating apoptotic-related diseases, including
C autoimmune disease, cancer, acquired immunodeficiency syndrome (AIDS),
C neurodegenerative diseases and ischaemic injury. The anti-caspase-14
C antibody is useful for measuring the level of caspase-14 in a tissue
C sample. An antibody that binds to a caspase-14 polypeptide is useful for
C isolating the polypeptide, and an antibody that binds to the large or
C small subunit the polypeptide is useful for identifying samples with
C caspase-14 processing activity. An antibody that binds to caspase-14
C heterodimer or heterotetramer is useful for isolating caspase-14 with
C apoptotic activity or in a screening assay to identify (ant)agonists. The
C antibodies form kits for such purposes. The anti-caspase-14 antibody is
C also useful for preparing anti-idiotypic antibodies, which mimic a
C caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
C the antibody is useful as a competitor of caspase-14 in reducing the
C level of caspase-14 activity, which reduces the level of apoptotic
C activity. Oligonucleotides made from the polynucleotides are useful as
C polymerase chain reaction (PCR) primers or probes to screen genomic or
C cDNA libraries for similar caspase-14 encoding polynucleotides, or for
C diagnosis of diseases associated with enhanced or inhibited apoptosis.
C The isolated caspase-14 gene permits methods of modulating apoptosis for
C the treatment of human diseases
X Q Sequence 281 AA;
Query Match 75.4%; Score 934.5; DB 2; Length 281;
Best Local Similarity 70.9%; Pred. No. 4.3e-89;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
Y 1 MSNPRLEEEKYDMSGALALILCVTKAREGSEEDLDALHEHFRQLRPFESTMKRDPTEAQ 60
Yb 24 MSDPQLQEERYDMSGARLALTLCVTKAREGSEVDMEALRMFRYLKFESTMKRDPTEAQ 83
Y 61 FOELEKFOAIDSDREDPVSCAFVLMHAGREGFLKGGEGEMVKLENLFEALNNKNCAL 120
Yb 84 FLEELDFEQTTIDNWEPEVSCAFVLMHAGREGGLKAGEDEKVRLEDLFEVLNNKNCAL 143
Y 121 RAKPKVYIIQACRGEQDPG-----ETVGGDEIVVMVKDSQPTIPTYTDALHV 168
Yb 144 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPNQSIPTYTDLHI 202
Y 169 YSTVEGVYIYRHDQKSCFTQTLVDVFTKRKHILLELLTEVTRMAEELVQEGKARKTN 228
Yb 203 YSTVEGVLSVRHDEKSGGFIQTLTDVFIHKKSILLETTEILTMANTVEVQEGFRKN 262
Y 229 PETQSTLRKLYLQ 242
Yb 263 FEVQSTLRKLYLQ 276

ID AAY93213 standard; protein; 281 AA.
XX AAY93213;
AC AAY93213;
XX 04-SEP-2000 (first entry)
DT Amino acid sequence of a murine caspase-14.
XX Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.
KW Mus sp.
XX Key Location/Qualifiers
FT Region 1..156 "large subunit"
FT Active-site 134..138
FT Cleavage-site 156..157
FT Cleavage-site 162..163
FT Region 163..257
FT /note= "small subunit"
XX WO200028047-A1.
PN 18-MAY-2000.
XX 29-OCT-1999; 99WO-US025523.
XX 06-NOV-1998; 98US-C0187789.
XX (UYJB-) UNIV JEFFERSON THOMAS.
XX Alnemri ES, Fernandez-Alnemri T;
XX WPI; 2000-376858/32.
XX N-PSDB; AAL15163.
XX Novel nucleic acids encoding cell death specific protease termed caspase-
PT 14 useful for treating cancers by stimulating apoptosis.
XX Claim 52; Fig 1; 78pp; English.
XX The present sequence represents a murine caspase-14 polypeptide. The
XX polypeptide is a cell death specific protease, and is an apoptosis
XX stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
XX -14 antibodies are useful for treating or reducing the severity of
XX pathological conditions associated with increased or decreased levels of
XX apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
XX diseases and ischemic injury are treated by administering anti-caspase-14
XX antibodies. The antibody is useful for determining the presence or the
XX level of caspase-14 in tissue sample and also for the isolation of
XX caspase-14 with apoptotic activity or in screening assay to identify an
XX agent that inhibits heterodimer or heterotetramer formation and
XX therefore, apoptosis
XX Sequence 281 AA;
Query Match 75.4%; Score 934.5; DB 3; Length 281;
Best Local Similarity 70.9%; Pred. No. 4.3e-89;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
Qy 1 MSNPRLEEEKYDMSGALALILCVTKAREGSEEDLDALHEHFRQLRPFESTMKRDPTEAQ 60
Db 24 MSDPQLQEERYDMSGARLALTLCVTKAREGSEVDMEALRMFRYLKFESTMKRDPTEAQ 83
Qy 61 FOELEKFOAIDSDREDPVSCAFVLMHAGREGFLKGGEGEMVKLENLFEALNNKNCAL 120
Db 84 FLEELDFEQTTIDNWEPEVSCAFVLMHAGREGGLKAGEDEKVRLEDLFEVLNNKNCAL 143
Qy 121 RAKPKVYIIQACRGEQDPG-----ETVGGDEIVVMVKDSQPTIPTYTDALHV 168
Db 144 RGKPKVYIIQACRGEHRDPGEELRGNEELGGDEELGGDE-VAVLKNPNQSIPTYTDLHI 202

169 YSTVEGYIAYRHDKGSCFIOTLVDFTKRGHILELLETTETRRMAEALVQSGKARKTN 228
203 YSTVEGYLSYRDEKSGSFIOTLVDFIHKKSILELTTETRLMANTENVQSGKPRKVN 262
229 PEIQSTLRKRLYLQ 242
263 PEVQSTLRKRLYLQ 276

RESULT 9
AY93215
J AAY93215 standard; protein; 230 AA.
K AAY93215;
L AAY93215;
M I 04-SEP-2000 (first entry)
N E Amino acid sequence of a human caspase-14 splice variant.
O X Caspase-14; cell death specific protease; apoptosis stimulator;
P W apoptosis; AIDS; neurodegenerative disease; ischemic injury.
S Homo sapiens.
X H Key Location/Qualifiers
I Active-site 130..134
N WO200028047-A1.
D 18-MAY-2000.
F 29-OCT-1999; 99WO-US025523.
K 06-NOV-1998; 98US-00187789.
R (UYJE-) UNIV JEFFERSON THOMAS.
A Alnemri ES, Fernandez-Alnemri T;
I WPI; 2000-376558/32.
R N-PSDB; AAA15165.
T Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
X Claim 41; Fig 8; 78pp; English.
S The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis

Query Match 71.8%; Score 890; DB 3; Length 230;
Best Local Similarity 99.4%; Pred. NO. 1.5e-84;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 MSNPSLEEKKYDMSGAALILCVTKAREGSEEDLDLEHMFRLRFEFTWKRDPTAEQ 60
b 1 MSNPSLEEKKYDMSGARLILCVTKAREGSEEDLDLEHMFRLRFEFTWKRDPTAEQ 60
Y 61 FQBELEKFOAIDSRDDPVSCAFVLMVMAHGRGFLKGEDGEMVKLENLFEALNNKCOAL 120
b 61 FQBELEKFOAIDSRDDPVSCAFVLMVMAHGRGFLKGEDGEMVKLENLFEALNNKCOAL 120

QY 121 RAKPKVIIQACRGEQDPGETVGGDEIVVMVKDSPQTIPTTDLALHVYSTVEG 174
DB 121 RAKPKVIIQACRGEQDPGETVGGDEIVVMVKDSPQTIPTTDLALHVYSTVEG 174

RESULT 10
AAU72882
ID AAU72882 standard; protein; 234 AA.
XX AAU72882;
AC AAU72882;
XX 26-FEB-2002 (first entry)
DT Human aspartyl protease partial protein sequence #7.
DE Human; protease; PCR primer; cytostatic; immunomodulator; cardiant;
XX vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser;
KW hypertensive; neuroleptic; neuroprotective; anabolic;
KW anorectic; antiinflammatory; aspartyl protease; cysteine protease; colon;
KW metalloprotease; serine protease; cancer; haematopoietic; breast; lung;
KW lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;
KW immune-related disease; cardiovascular disease; neuronal disease;
KW migraine; sexual dysfunction; mood disorder; attention disorder;
KW cognition disorder; hypotension; hypertension; psychotic disorder;
KW dyskinesia; metabolic disorder; inflammatory disorder.
XX Homo sapiens.
OS WO200183782-A2.
XX 08-NOV-2001.
PD 04-MAY-2001; 2001WO-US014431.
XX 04-MAY-2000; 2000US-0201879P.
PF (SUGE-) SUGEN INC.
XX Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Payne V;
XX WPI; 2002-041502/05.
DR N-PSDB; AAS97165.
XX Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory disorders.
PT Claim 28; Fig 2A; 232pp; English.
XX The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoietic origin, of the breast, colon, lung, prostate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAU72876-AAU72910 represent human protease amino acid sequences of the invention

Sequence 234 AA;
Query Match 38.1%; Score 472.5; DB 5; Length 234;
Best Local Similarity 45.0%; Pred. NO. 8.1e-41;
Matches 107; Conservative 47; Mismatches 73; Indels 11; Gaps 7;

11 KYDMSGAALAILCVTKAREGSEEDLDALHMFROLRPFSTMKRDPRTAEQFOEELKFOQ 70
1 QYDLSKRAALLAVLQGRPGAGHVEALGGLCWALGFETTVTRPTTAQAEELAQFRE 60
71 AIDSREDPVSCAFVWLMAH-GREGFLKGBDEGMVKLENLFEALNNKNCQALRAKPKVII 129
61 QLDTCRGPVSCALVALMAHGGPRGQLLGADGQEVQPEALMQELS--RCQVLQGRPKIFLL 118
130 QACRGQRDPGETVGGDEIVMWIK--DSPQTPTVTDALHVVSTVEGYAYRHDKQGSCEF 187
119 QACRGGRNDAG--VGPTALPWWSWLRAPPSVPSHADVLQIYAEAGGVAYR-DDKGSDF 175
188 IQTLVDVFTKRKGH-ILELLTEVTRMAEALVQEE--GKARTNPEIOTSLRKRLYLQ 242
176 IQTLVEVLNRPGRDLELLTEVNRVRCQEVGLGPCDELKACLEIRSSLRRLCLQ 233

RESULT 11

BG76499
D ABG76499 standard; protein; 398 AA.
X C ABG76499;
X X
X 05-NOV-2002 (first entry)
X X

DNA encoding protein modification and maintenance molecule #3.

Protein modification and maintenance molecule; gastrointestinal disorder;
dysphagia; esophageal spasm; gastritis; anorexia; nausea; hypertension;
cardiovascular disorder; atherosclerosis; vasculitis; aneurysm; allergy;
ischemic heart disease; autoimmune disorder; inflammatory disorder;
acquired immunodeficiency syndrome; AIDS; ankylosing spondylitis; cancer;
anemia; amyloidosis; cell proliferative; arteriosclerotic burstis;
cirrhosis; developmental disorder; renal tubular acidosis; ananemia;
bone resorption; epilepsy; epithelial disorder; keratosis pilaris;
allergic contact dermatitis; insect bite; keloid; dermatofibroma; eczema;
neurological disorder; stroke; cerebral neoplasm; Alzheimer's disease;
Huntington's disease; dementia; reproductive disorder; infertility;
endometriosis; gynecomastia; ectopic pregnancy; gene therapy.

Homo sapiens.

WO200260942-A2.
X X
X 08-AUG-2002.
X X
X 30-JAN-2002; 2002WO-US002813.
X X
X 31-JAN-2001; 2001US-0265705P.
X X
X 05-FEB-2001; 2001US-0266762P.
X X
X 16-FEB-2001; 2001US-0269581P.
X X
X 23-FEB-2001; 2001US-0271198P.
X X
X 01-MAR-2001; 2001US-0272813P.
X X
X 13-MAR-2001; 2001US-0275586P.
X X
X 23-MAR-2001; 2001US-0278505P.
X X
X 30-MAR-2001; 2001US-0280539P.

(INCY-) INCYTE GENOMICS INC.

Warren BA, Honchell CD, Lu Y, Wallia NK, Burford N, Delegeane AM;
Gandhi AR, Baugun MR, Griffin JA, Gietzen KJ, Lu DM, Ison CH;
Ranikumar J, Tang TY, Lal PG, Borowski M, Duggan BM, Hafalia AJA;
Arvizu C, Thangavelu K, Yao MG, Elliott VS, Ding L, Yue H, Lee S;
Swarnakar A, Tran UK, Xu Y;
WPI, 2002-608499/65.
X X
X N-PSDB; ABS58370.
X X

New protein modification and maintenance molecules useful for treating or
preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
cell proliferative, developmental, neurological and reproductive
disorders.

PS Claim 1; Page 133-134; 172pp; English.
XX
CC The invention describes an isolated human polypeptide (I), a naturally
CC occurring amino acid sequence at least 90 % identical to the protein, or
CC a biologically active fragment or an immunogenic fragment of the protein.
CC The protein modification and maintenance molecules are useful in the
CC diagnosis, treatment, and prevention of gastrointestinal (e.g. dysphagia,
CC esophageal spasm, gastritis, anorexia or nausea), cardiovascular (e.g.
CC atherosclerosis, hypertension, vasculitis, aneurysms, or ischaemic heart
CC disease), autoimmune/inflammatory (e.g. acquired immunodeficiency
CC syndrome (AIDS), allergies, ankylosing spondylitis, anaemia or
CC amyloidosis), cell proliferative (e.g. cancers, arteriosclerotic,
CC burstis, or cirrhosis), developmental (e.g. renal tubular acidosis,
CC anaemia, bone resorption, or epilepsy), epithelial (e.g. allergic contact
CC dermatitis, keratosis pilaris, insect bites, keloid, dermatofibroma or
CC eczema), neurological (e.g. stroke, cerebral neoplasms, Alzheimer's
CC disease), Huntington's disease or dementia), and reproductive disorders
CC (e.g. infertility, endometriosis, gynecomastia or ectopic pregnancy).
CC These may also be used in assessing the effects of exogenous compounds on
CC the expression of nucleic acid and amino acid sequences of protein
CC modification and maintenance molecules. Polynucleotides are useful in
CC somatic and germline gene therapy. This is the amino acid sequence of a
CC protein modification and maintenance molecule described in the invention
XX
X X Sequence 398 AA;

Query Match 38.1%; Score 472.5; DB 5; Length 398;
Best Local Similarity 45.0%; Pred. No. 1.7e-40;
Matches 107; Conservative 47; Mismatches 73; Indels 11; Gaps 7;
QY 11 KYDMSGAALAILCVTKAREGSEEDLDALHMFROLRPFSTMKRDPRTAEQFOEELKFOQ 70
Db 165 QYDLSKRAALLAVLQGRPGAGHVEALGGLCWALGFETTVTRPTTAQAEELAQFRE 224
QY 71 AIDSREDPVSCAFVWLMAH-GREGFLKGBDEGMVKLENLFEALNNKNCQALRAKPKVII 129
Db 225 QLDTCRGPVSCALVALMAHGGPRGQLLGADGQEVQPEALMQELS--RCQVLQGRPKIFLL 282
QY 130 QACRGQRDPGETVGGDEIVMWIK--DSPQTPTVTDALHVVSTVEGYAYRHDKQGSCEF 187
Db 283 QACRGGRNDAG--VGPTALPWWSWLRAPPSVPSHADVLQIYAEAGGVAYR-DDKGSDF 339
QY 188 IQTLVDVFTKRKGH-ILELLTEVTRMAEALVQEE--GKARTNPEIOTSLRKRLYLQ 242
Db 340 IQTLVEVLNRPGRDLELLTEVNRVRCQEVGLGPCDELKACLEIRSSLRRLCLQ 397

RESULT 12

ABBI0110
ID ABBI0110 standard; protein; 452 AA.
XX
AC ABBI0110;
XX
DT 26-JUN-2002 (first entry)
XX
DE Mouse caspase 2 protein.
XX
KW Caspase 2; antitense; cytostatic; osteopathic; cerebroprotective;
KW neuroprotective; antilipemic; antiinflammatory; antimicrobial;
KW haematopoietic disorder; bone metabolism disorder; cholesterol disorder;
KW hyperproliferative disorder; cancer; blood disorder; stroke;
KW brain injury; neurodegenerative disease; infection; inflammation; tumour.
OS Mus musculus.
XX
XX WO200224720-A1.
XX
XX 28-MAR-2002.
XX
XX 14-SEP-2001; 2001WO-US028631.
XX
XX 20-SEP-2000; 2000US-00667018.
XX

A (ISIS-) ISIS PHARM INC.

X Zhang H, Watt AT;

X WPI; 2002-351998/38.

R R N-PSDB; ABB58563.

X T New antisense compounds targeted to nucleic acid molecule encoding
T caspase 2, useful for treating diseases or conditions associated with
T caspase 2, e.g. cancer, blood disorders, stroke, brain injury and
T neurodegenerative diseases.

X Example 13; Page 111-113; 146pp; English.

X C The invention relates to a compound 8-50 nucleobases in length targeted
C to a nucleic acid molecule encoding caspase 2, which specifically
C hybridises with and inhibits the expression of caspase 2, or specifically
C hybridises with at least an 8-nucleobase portion of an active site on a
C nucleic acid molecule encoding caspase 2. The activity of antisense
C oligonucleotides of the invention may be described as, cytostatic,
C osteopathic, cerebrotective, neuroprotective, antilipemic,
C antiinflammatory and antimicrobial. The antisense compounds are useful
C for treating an animal having a disease or condition associated with
C caspase 2, such as haematopoietic disorder, bone metabolism disorder,
C cholesterol disorder, or a hyperproliferative disorder. These compounds
C may further be used as research reagents and diagnostics, to distinguish
C between functions of various members of a biological pathway, in the
C treatment of a disease or disorder which can be treated by modulating the
C expression of caspase 2, including cancer, blood disorders, stroke, brain
C injury and neurodegenerative diseases. They may also be used for tumour
C prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
C formation. The current sequence represents the mouse caspase 2 protein

X Q Sequence 452 AA;

Query Match 23.8%; Score 295; DB 5; Length 452;

Best Local Similarity 31.5%; Pred. No. 8.2e-22;

Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Y 29 REGSEEDLDALHMFQRLRFESTMKRDPATAEQFOEELKFOQAIDSRDVPSCAFVVLMA 88

b 219 RSGGDVHTTTLVTLFKLGYNVHVLHDQTAQEMQEKLNFAQ-LPAHRVTDSCV-VALLS 276

Y 89 HGREGLKGDGEWVKLENLFEALNNKCOALRAKPKVYIIQACRGEORDPG----- 140

b 277 HGVEGGIYVDGKLLQQLQGVFLFNANCPSLQNKPMFFIQAACRGDETRDGVDDQDGKN 336

Y 141 -----ETVGGDEIVMVKDSPQTIPTTYTDALHVTSTVEGYIAYRHDKGSCFIQTLV 192

b 337 HTQSPGCEESDAGKEELMKMR-----LPTRSDMTCGYACKLGNAAAMNTKRGSWYIEALT 391

Y 193 DVFTKR--KGHILELLTEVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241

b 392 QVFSERACDMHVADMLVKVNALIKE-----REGYAPGTEFHRCKEMSEYCSLTCCQLYL 445

RESULT 13

ADB79812

D ADB79812 standard; protein; 452 AA.

X ADB79812;

X 04-DEC-2003 (first entry)

X Rat caspase 2, Ich-1, SEQ ID 52.

X Analgesic; pain; streptozocin-induced diabetes; rat.

X Rattus norvegicus.

X EPI279744-A2.

X 29-JAN-2003.

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26-JUL-2002; 2002EP-00255249.

27-JUL-2001; 2001GB-00018354.

07-FEB-2002; 2002GB-00002910.

(WARN) WARNER LAMBERT CO.

Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

WPI; 2003-395407/38.

N-PSDB; ADE79813.

Use of isolated gene sequences and encoded polypeptides that are

upregulated in the spinal cord in response to streptozocin-induced

diabetes for screening compounds for the treatment of pain, or for

diagnosing pain.

Claim 1; Page 115-117; 334pp; English.

The present invention relates to nucleotide sequences which are useful in

the screening of compounds for the treatment of pain, or for the

diagnosis of pain. The nucleotide sequences are up-regulated in the

spinal cord in response to streptozocin-induced diabetes. The present

sequence was used to illustrate the invention.

Sequence 452 AA;

Query Match 23.6%; Score 293; DB 7; Length 452;

Best Local Similarity 31.5%; Pred. No. 1.3e-21;

Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Q 29 REGSEEDLDALHMFQRLRFESTMKRDPATAEQFOEELKFOQAIDSRDVPSCAFVVLMA 88

b 219 RSGGDVHTTTLVTLFKLGYNVHVLHDQTAQEMQEKLNFAQ-LPAHRVTDSC-IVALLS 276

Q 89 HGREGLKGDGEWVKLENLFEALNNKCOALRAKPKVYIIQACRGEORDPG----- 140

b 277 HGVEGGIYVDGKLLQQLQGVFLFNANCPSLQNKPMFFIQAACRGDETRDGVDDQDGKN 336

Q 141 -----ETVGGDEIVMVKDSPQTIPTTYTDALHVTSTVEGYIAYRHDKGSCFIQTLV 192

b 337 HAQSPGCEESDAGKEELMKMR-----LPTRSDMTCGYACKLGNAAAMNTKRGSWYIEALT 391

Q 193 DVFTKR--KGHILELLTEVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241

b 392 QVFSERACDMHVADMLVKVNALIKE-----REGYAPGTEFHRCKEMSEYCSLTCCQLYL 445

RESULT 14

ADB63000

ID ADE63000 standard; protein; 452 AA.

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

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XX ADE63000;

XX ADE63000;

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XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX ADE63000;

XX (GHEO) GEN HOSPITAL CORP.
 2A (FAEB) BAYER AG.
 XX
 21 Woolf C, D'urso D, Befort K, Costigan M;
 2R WPI; 2003-268312/26.
 2X GENBANK; AAB96379.
 2R
 2T New composition comprising two or more isolated polypeptides, useful for
 2T preparing a medicament for treating pain in an animal.
 2X
 2S Claim 1; Page; 1017pp; English.
 2X
 2X The invention discloses a composition comprising two or more isolated rat
 2X or human polynucleotides or a polynucleotide which represents a fragment,
 2X derivative or allelic variation of the nucleic acid sequence. Also
 2X claimed are a vector comprising the novel polynucleotide, a host cell
 2X comprising the vector, a method for identifying a nucleotide sequence
 2X which is differentially regulated in an animal subjected to pain and a
 2X kit to perform the method, an array, a method for identifying an agent
 2X that increases or decreases the expression of the polynucleotide sequence
 2X that is differentially expressed in neuronal tissue of a first animal
 2X subjected to pain, a method for identifying a compound which regulates
 2X the expression of a polynucleotide sequence which is differentially
 2X expressed in an animal subjected to pain, a method for identifying a
 2X compound that regulates the activity of one or more of the
 2X polynucleotides, a method for producing a pharmaceutical composition, a
 2X method for identifying a compound or small molecule that regulates the
 2X activity in an animal of one or more of the polypeptides given in the
 2X specification, a method for identifying a compound useful in treating
 2X pain and a pharmaceutical composition comprising the one or more
 2X polypeptides or their antibodies. The polynucleotide or the compound that
 2X modulates its activity is useful for preparing a medicament for treating
 2X pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 2X injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 2X therapy). The sequence presented is a rat protein (shown in Table 2 of
 2X the specification) which is differentially expressed during pain. Note:
 2X The sequence data for this patent did not form part of the printed
 2X specification, but was obtained in electronic form directly from WIPO at
 2X ftp.wipo.int/pub/published_pct_sequences.
 2X
 2X Sequence 452 AA;

Query Match 23.6%; Score 293; DB 7; Length 452;
 Best Local Similarity 31.5%; Pred. No. 1.3e-21;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;
 29 REGSEEDLDALHEMFRLQRFESTMKRDPETAQFOBELEKFOQAIDSREDPVSCAFVVLMA 88
 219 RSGGDVHTTLVTLFKLLGYNVHVLYDQTAQEMQKLNFAQ-LPAHRVTDSC-IVALLS 276
 89 HGREGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
 277 HGVEGGYVGDGKLLQLOEYFRFDNANCPSLQNKPKMFFIQACRGEDETRGVDDQDGKN 336
 141 -----ETVGGDEIVMWIKDSPQTIPTVTDALHVIYSTVEGVIAYRHDKGSCFIQTLV 192
 337 HAQSPGCEESDAGKEMLMKR-----LPTSDMICGYACLGKNAAMRNTKRGSWYIEALT 391
 193 DVPTKR--KGHILELLETVTRMAEELVQSGKARKTN-----PEIQSTLRKRLYL 241
 392 QVFSERACDMHVADMLVKVNALIKE----REGYAPGTGFHRCKEMSEYCVSTLCQQLYL 445

RESULT 15
 AAR66771
 D AAR66771 standard; protein; 435 AA.
 X
 X AAR66771;

T 25-MAR-2003 (revised)
 T 13-SEP-1995 (first entry)

XX Human interleukin-1 beta converging enzyme ced 3 homolog Ich-1(L).
 DE
 XX
 KW Human interleukin-1 beta converging enzyme ced 3 homolog; Ich-1(L);
 KW oncogene bcl-2; programmed cell death; cancer treatment.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Active-site 301..305
 XX WO9500160-A1.
 XX
 XX 05-JAN-1995.
 XX
 XX 10-JUN-1994; 94WO-US006630.
 XX
 XX 24-JUN-1993; 93US-00080850.
 XX (GHEO) GEN HOSPITAL CORP.
 XX
 XX Yuan J, Miura M;
 XX WPI; 1995-051742/07.
 XX N-PSDB; AAR679971.
 XX
 XX or preventing programmed cell death in vertebrate cells - by inhibiting
 XX the activity of interleukin-1 beta converting enzyme.
 XX
 XX Example 5; Fig 12A; 116pp; English.
 XX
 XX AAR679971 encodes AAR66771 human interleukin-1 beta converting enzyme ced
 XX 3 homolog Ich-1(L), increasing Ich-1(L)s enzymatic activity can promote
 XX the programmed cell death of cancer cells (pref. those overexpressing the
 XX bcl-2 oncogene), this can be used as the basis of a new cancer treatment.
 XX Alternatively by reducing Ich-1(L)s enzymatic activity programmed cell
 XX death can be inhibited, this may be useful in the development of new cell
 XX lines which remain viable in culture for extended or indefinite periods,
 XX independent of growth factors. (Updated on 25-MAR-2003 to correct FN
 XX field.)
 XX
 XX Sequence 435 AA;

Query Match 23.3%; Score 289; DB 2; Length 435;
 Best Local Similarity 31.1%; Pred. No. 3.3e-21;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
 29 REGSEEDLDALHEMFRLQRFESTMKRDPETAQFOBELEKFOQAIDSREDPVSCAFVVLMA 88
 202 RSGGDVHTTLVTLFKLLGYNVHVLYDQTAQEMQKLNFAQ-LPAHRVTDSC-IVALLS 259
 89 HGREGFLKGEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
 260 HGVEGGYVGDGKLLQLOEYFRFDNANCPSLQNKPKMFFIQACRGEDETRGVDDQDGKN 319
 141 -----ETVGGDEIVMWIKDSPQTIPTVTDALHVIYSTVEGVIAYRHDKGSCFIQTLV 192
 320 HAQSPGCEESDAGKE-----KLPMKRLPTRSDMICGYACLGKNAAMRNTKRGSWYIEALA 374
 193 DVPTKR--KGHILELLETVTRMAEELVQSGKARKTN-----PEIQSTLRKRLYL 241
 375 QVFSERACDMHVADMLVKVNALIKD----REGYAPGTGFHRCKEMSEYCVSTLCRHLVL 428

Search completed: March 19, 2004, 11:22:15
 Job time : 50.1713 secs